



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96572

TO: Gary Nickol
Location: cm-1/8d17/8e12
Art Unit: 1642
Friday, June 20, 2003

Case Serial Number: 513365

From: Mona Smith
Location: Biotech-Chem Library
CM1-6A01
Phone: 308-3278

mona.smith@uspto.gov

Search Notes

Thank you for using STIC services
Feel free to contact me if you have any questions.

Mona Smith
308-3278

STIC-Biotech/ChemLib

96592

From: Nickol, Gary
Sent: Friday, June 13, 2003 3:56 PM
To: STIC-Biotech/ChemLib
Subject: 09/513365

Please search the following:

- 1) DNA of SEQ ID NO:2
- 2) DNA encoding the amino acids of SEQ ID NO:1

Thanks,

Gary Nickol
CM1, AU:1642
Room 8D17, Mailbox 8E12
(703) 305-7143

RECEIVED
JUN 13 2003
(STIC)

Searcher: M. Smith
Phone: _____
Location: _____
Date Picked Up: 6/16/03
Date Completed: 6/20/03
Searcher Prep/Review: 4
Clerical: 5
Online time: 5

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 20, 2003, 02:40:48 ; Search time 1428 seconds

(without alignments)
3175.586 Million cell updates/sec

Title: US-09-513-365a-1

Perfect score: 1481

Sequence: 1 MLCGQQQQQLYSSAALLTGER.....DNKTKMDKSTKTKKDRRSR 280

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=zip
-Q/cgna2_1/USFTO.spool/US09513365/runat_16062003_124743_16453/app_query.fasta.1.455
-DB=EST-QPWT-fastap -SOFTX=1 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-Biosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=500 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09513365 -CGN_1_1_2874 -runat_16062003_124743_16453 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEODDERY -NBS_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthum:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395.5	94.2	1464	11 AK012716	AK012716 Mus musculus
2	1296	87.5	912	14 BQ277444	BQ277444 AGENCOURT
3	1096.5	74.0	919	12 BG211544	BG211544 RST31111
4	1094	73.9	793	12 BE796780	BE796780 601587557
5	1063	71.8	778	13 B1548536	B1548536 603191255
6	1024	69.1	735	14 BM982877	BM982877 UT-CF-EN1
7	1006.5	68.0	798	12 BG184056	BG184056 RST2972 A
8	961	64.9	664	14 BM719460	BM719460 UT-E-EJ1
9	935	63.1	708	13 B1460319	B1460319 603201967
10	920	62.1	675	14 BM682789	BM682789 UT-E-EJ1
11	902	60.9	891	13 B1091047	B1091047 602855235
12	897	60.6	541	12 BF114684	BF114684 7166C08.X
13	889	60.0	679	10 AV647917	AV647917 AV647917
14	883	59.6	564	12 BE839427	BE839427 RC3-FN014
15	874	59.0	538	12 BF523624	BF523624 UT-R-C1-1
16	864	58.3	653	13 B1495873	B1495873 df121d04
17	856	57.8	522	13 B1495874	B1495874 df121d04
18	852	57.5	566	12 BE839460	BE839460 RC3-FN014
19	849	57.3	720	9 AA797495	AA797495 vW2B01.T
20	847	57.2	703	13 B1546850	B1546850 603189754
21	830	56.0	531	9 AA204672	AA204672 zrf8C06.T
22	829	56.0	525	9 A1885642	A1885642 w159h01.X
23	814	55.0	616	9 AL673816	AL673816 AL673816
24	805	54.4	547	9 A186701	A186701 qe82d12.X
25	798	53.9	482	12 BE831862	BE831862 RC6-MT006
26	780	52.7	692	9 AL633536	AL633536 AL633536
27	779.5	52.6	830	12 BG189892	BG189892 RST8946 A
28	775	52.3	601	14 BQ206861	BQ206861 UT-M-D21
29	766	51.7	844	12 BG862842	BG862842 602797509
30	762	51.5	975	14 BQ934291	BQ934291 AGENCOURT
31	760	51.3	513	9 A1857399	A1857399 w155f09.X
32	745	50.3	537	9 A1458721	A1458721 TK13h10.X
33	741	50.0	574	10 A6674408	A6674408 ba59f06.X
34	730	49.3	873	14 BQ430264	BQ430264 AGENCOURT
35	728	49.2	460	10 A6674790	A6674790 ba59f06.Y
36	724	48.9	561	13 BJ098630	BJ098630 BJ098630
37	709	47.9	482	9 AA746304	AA746304 oa36d03.T
38	700.5	47.3	609	10 AW342872	AW342872 IJ80d12.Y
39	697	47.1	475	10 BE653650	BE653650 UT-M-AH1
40	692	46.7	477	12 BF513151	BF513151 UT-H-BM1
41	690	46.6	555	14 BQ033210	BQ033210 UT-1-CFO-
42	688	46.5	502	12 BF732679	BF732679 nsg05d11
43	682	46.0	520	13 B1676689	B1676689 iCS3d06.X
44	681.5	46.0	442	9 AL118087	AL118087 r2225a08
45	681	46.0	466	9 A1818729	A1818729 wk91d10.X

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	1464 bp	MRNA	linear	HTC 19-JAN-2002
AK012716	AK012716	Mus musculus 10, 11 days embryo whole body				
ACCESSION	AK012716	sequence.				
VERSION	AK012716.1	GI:12849649				
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (strain: C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone: 2810011M06.					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
99279293
10349636
2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
AUTHORS

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumai, T., Teshiro, H., Itoh, M., Suni, R., Ishii, T., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashinagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiria, A. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
20499374
11042159
4

Riken integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicephillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE
AUTHORS

4

Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Itawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, K., Saito, T., Okazaki, Y., Gojodori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuhl, P., Lewis, S., Matsuo, Y., Nikolaio, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stamboli, F., Suzuki, R., Tomita, M., Wagner, E., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Bozell, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Butt, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hotmanom, L., Hume, D.A., Kamuya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombers, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakemoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, T., Kawaji, H., Kottuski, S. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
21085651
11217851
5 (bases 1 to 1464)

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

REFERENCE
AUTHORS

5 (bases 1 to 1464)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Butt, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiroka, T., Horii, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koza, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numata, K., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriner, L., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Soabebe, Y., Suzuki, H., Tagami, M., Tadaga, A., Takahashi, F., Tanaka, T., Teijma, Y., Toya, T., Yamamura, T., Yananaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
Submitted (10-JULY-2000)

Direct Submission
Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,

COMMENT
 Fax: 81-45-503-9216)
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGACAGCTCTCTTTTCTTTTCTTTTAA 3'], cDNA was prepared by using triethanolamine-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCCAGTAAATTAATTAATTCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES
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 /db_xref="MG:1901365"
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 /clone="2810011M06"
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 /dev_stage="10, 11 days embryo"
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 similar to P33ING2"
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 Score: 1395.50 Matches: 269
 Percent Similarity: 97.86% Conservative: 6
 Best local Similarity: 95.73% Mismatches: 5
 Query Match: 94.23% Indels: 2
 Gaps: 11
 US-09-513-365A-1 (1-280) x AK012716 (1-1464)
 Oy 1 Metleugly---GlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThGlyGlu 19
 Db 478 ATGTTAGGGGCGAGCGACGACACACAGCTGACTGCTGGCGGCTCTTACCGGAG 537
 Oy 20 ArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGlnCysValGlnSerLeuPro 39
 Db 538 CGGAG-CGGCGCTCTCTCTCTCTAGCTGAGGACATCACTGAGAGTGCTGGATCTGCTGCC 596
 Oy 40 HisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThr 59
 Db 597 CACGACATGCGAGAGAACGTCTCGCTGCTGCGGAGCTGGCAACAATACCAAGAAACG 656
 Oy 60 LeuIysGlnIleAspAspValTyrGlnLysTyrLysLysGlnAspAspLeuAsnGlnLys 79
 Db 657 TTAAAGGAATATGATGATGCTCTATGAAATAATAGAAAGAGATGATTCACACAGAA 716

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QY 80 LysArgLeuGlnGlnLeuGlnArgAlaLeuIleAsnSerGlnGluGlyAspGlu 99
DB 717 AAAGCCTACAGAGCAATCTCCAGAGCGTTATCATAGCCAAAGATTCGGAGATGAA 776
QY 100 LysIleGlnIleValThrGlnMetLeuGlnValGlnAsnArgAlaArgGlnMetGlu 119
DB 777 AAAATTGATGTCACACGAGATGCTCGAATTGGTGGAAGAACCGAGGAGCAAAATGAG 836
QY 120 LeuHisSerGlnCysPheGlnAspProAlaGlnSerGlnArgAlaSerAspGlnAlaGly 139
DB 837 CTGCATTCACAGATGTTTCAGAGATCTGCTGAAGATGAGCGAGCTCGACAAATCGAAG 896
QY 140 MetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlu 159
DB 897 ATGATTCACAGTCAACCGAAGATCTTCTGAAGACCTCGAAGACAGAGACCAAGTGGAG 956
QY 160 SerArgAspLeuGlnCysHisMetAlaAsnGlyIleGlnAspCysAspAspGlnProProlys 179
DB 957 AGCCGTACTTATGTCACATGACAAACGGGATTCAGACACTGTGATTCACACCGGAAA 1016
QY 180 GluIleLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGlu 199
DB 1017 GAAAGAGATTCACAGATCCCGCAAGAGAGAGAGCGCTCCAGCGCCAGAGAGAGAGGAG 1076
QY 200 AlaSerProValGluPheAlaIleAspProAsnGlnProThrTyrCysLeuGln 219
DB 1077 GCATCCCTGTCGAGTTCGATTCGATCCCAATGAGCCACCTACTGCTTGTAACCA 1136
QY 220 ValSerTyrGlnGluMetIleGlyCysAspAsnGlnGlnCysProIleGluThrPheHis 239
DB 1137 GTGTCCTACGGGGAGATGATAGCTGTGACAAATGACAAAGTCTCCATTTGAATGGTTTCC 1196
QY 240 PheSerCysValSerIleThrTyrLysProLysGlyLysTyrPyrCysProLysCysArg 259
DB 1197 TTTTCATGCTGTTTACCTACCTATTAACCCCAAGGGAAATGCTTTGCCCAAGTGTGAG 1236
QY 260 GlyAspAsnGlnLysThrMetAspLysSerThrGluLysThrLysAspArgArgSer 279
DB 1257 GGAGACAAATGAGAAACCATGACGAAAGTACGCAAAAGACAAAAGAGAGAGAGAGCG 1316
QY 280 Arg 280
DB 1317 AGG 1319

RESULT 2
LOCUS BQ277444 912 bp mRNA linear EST 07-MAY-2002
DEFINITION AGENCOURT_6738254 NIH_MGC_127 Homo sapiens CDNA clone IMAGE:5810745
ACCESSION BQ277444
VERSION BQ277444.1 GI:20487652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 912)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapsb-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMN at:
http://image.llnl.gov
Plate: LICM2058 row: h column: 10
High quality sequence stop: 587.
FEATURES
Source 1..912

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/organism="Homo sapiens"
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/clone_lib="NIH_MGC_127"
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/lab_host="DH10B (T1-phage-resistant)"
/notes="Vector: pDNR-LIB; Site: 1: SfiI (ggccattagcc);
Site: 2: SfiI (ggccgcctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AACGATGCTGTCACGACGAGTCCATTCAGCCGCGG-3' and
5'-ATTCTAGAGCGCGGCGCGGCGGACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 1-2 kb
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_128). Library created in the laboratory of T.
Wedin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
Library."
BASE COUNT 313 a 184 c 235 g 180 t
ORIGIN
Alignment Scores:
Pred. No.: 1..1e-100 Length: 912
Score: 1296.00 Matches: 261
Percent Similarity: 92.71% Conservative: 6
Best Local Similarity: 90.62% Mismatches: 11
Query Match: 87.51% Indels: 11
DB: 14 Gaps: 1
US-09-513-365a-1 (1-280) x BQ277444 (1-912)
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DB 22 ATGTAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 81
QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGlnCysValGlnSerLeuProHis 40
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QY 41 AspMetGlnArgAsnValSerValLeuArgGlnLeuAspAsnLysTyrGlnGlnThrLeu 60
DB 142 GACATGACAGAGAAAGTGTCTGTCTGCGAAGCTGGCAACAATATCAAGAAACGTTA 201
QY 61 LysGlnIleAspAspValTyrGlnLysTyrLysGlnAspAspLeuAsnGlnLysLys 80
DB 202 AAGCAAAATGATGATGCTCTACGAAATATTAAGAAAGAGATGTTTAAACCAAGAGAA 261
QY 81 ArgLeuGlnGlnLeuGlnArgAlaLeuIleAsnSerGlnGluGlyAspGlnLys 100
DB 262 CGCTACAGCAGCTTCTCCACAGAGACACTAATTAATAGTCAAGATTTGGAGATCAAAA 321
QY 101 IleGlnIleValThrGlnMetLeuGlnLeuValGlnAsnArgAlaArgGlnMetGlnLeu 120
DB 322 ATACAGATGTTTACCAATCTCGAATGTGTGAATAATGGGCAAGCAAAATGAGTTA 381
QY 121 HisSerGlnCysPheGlnAspProAlaGlnSerGlnArgAlaSerAspGlnAlaGly 140
DB 382 CACTCAGAGTCTTCCAAAGATCCGCTGAAGTGAAGAGCTCGAGTAAAGCAAAAGTGG 441
QY 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlnSer 160
DB 442 GATTCACGACCAACCAAGAGATCTTCAAGAGACCCGACGAGCGGAGCAAGCAAGC 501
QY 161 ArgAspLeuGlnCysHisMetAlaAsnGlyIleGlnAspCysAspAspGlnProProlys 180
DB 502 CGTATTTATGTCACATGCGCAAAATGAGATTTGAAGACTGTGATGATCCACCTTAAGAA 561
QY 181 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200

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Db      562 AAGAAATCCAGTCAGCAAGAAAGAAACGCTCCAAAGGCAAGCAAGCAAGCAAGCAAGCT 621
QY      201 SerProValGluIleuHeaAlaIleaspProAsnGluProThyTyrCysLeuCysAsnGlnVal 220
Db      622 TCACCGTGTAGTTTCCAAATGATCCCTAAAGAACTACATACGCTTATCCAAACCCAGTGT 681
QY      221 SerTyrGluIleuMetIleGlyCysAspAsnGluGlyCysProIleGluTyrPheHis-Ph 240
Db      682 TCTATGCGGAGATGATAGATGTGACAAATGA-CAGGTCCCAATGATGATGGTTCACCTTT 740
QY      240 eSerCysValSerLeuThyTyrIlys-ProLysGlyIysTyrPyr-CysProLysCysArg 259
Db      741 TTCATGTGCTTCACTTACCTATTAACCCAAAGGGAATGCTATTGTCACCAAGTGCAGG 800
QY      260 -GlyAspAsn-----GluTyrThrMetAspLysSerThrGluIysThr 273
Db      801 GGAGATTAATGAGAAACCAACGAGCAAAAGTACTGTGAAAGAGCAACCAAAAGCAAA 860
QY      273 rLysLysAspArgArg 278
Db      861 TAGAAAAGATCCAAAG 876

RESULT 3
LOCUS   BG211544                      919 bp  mRNA  linear  EST 21-APR-2001
DEFINITION RST31111 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG211544
VERSION   BG211544.1 GI:13733231
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
          Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
          Lerner,L., Costanzo,D., McElligott,K., Boozier,S., Mays,R., Smith
          ,E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher
          ,J., Danzig,J. and Ducar,M.
          Creation of genome-wide protein expression libraries using random
          activation of gene expression
          Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
JOURNAL COMMENT Contact: Scott J. Cain
          Athersys, Inc.
          3201 Carnegie Ave, Cleveland, OH 44115, USA
          Tel: 216 431 9800
          Fax: 216 361 9596
          Email: scain@athersys.com
          High quality sequence stop: 439.
          Location/Qualifiers
            1. 919
FEATURES
source
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    /db_xref="taxon:9606"
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    /cell_line="HT1080"
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    Libraries using Random Activation of Gene Expression',
    Nature Biotechnology, in press. Note that even though the
    cell type indicated is HT1080, since a random activation
    method was used, these sequence tags are not necessarily
    expressed in HT1080 under normal circumstances."
BASE COUNT 332 a 151 c 216 g 216 t 4 others
ORIGIN
Alignment Scores:
Pred. No.: 1.04e-83 Length: 919
Score: 1096.50 Matches: 214
Percent Similarity: 96.00% Conservative: 2
Best Local Similarity: 95.11% Mismatches: 7
Query Match: 74.04% Indels: 4
DB: 12 Gaps: 1

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US-09-513-365a-1 (1-280) x BG211544 (1-919)
QY      58 GluThrLeuLysGluIleaspAspValTyrGluLysTyrIysGluAspAspLeuAsn 77
Db      4 GAAACCTTAAAGCAAAATGATGATGCTCTACGAAAAATATAGAAAGATGATTTAAAC 63
QY      78 GluLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuLeuSerGlnGlnLeuGly 97
Db      64 CAGAGAAACGCTTACAGCAGCTTCTCCAGAGCGCACTAATTAATGTCAGAAATGGGA 123
QY      98 AspGluLysIleGlnIleValThrGlnMetLeuGlnLeuValGluAsnArgAlaArgGln 117
Db      124 GATGAATAAATATACAGATTGTTACACAATAATCTCGAATTTGGTGAATAATCGGCAAGCAA 183
QY      118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerLysLysArgAlaSerAsp 137
Db      184 ATGAGATTACACACAGAGTGTTCAGAGATCCCTGCTGAAAGTAAAGACGAGCTCAGATTAA 243
QY      138 AlaLysMetAspSerSerGlnProGluArgSerSerArgArgProArgGlnArgThr 157
Db      244 GCAAGATGATTCAGCCACCAAGAAAGATCTTCAGAAAGACCCGACGACGAGC 303
QY      158 SerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnPro 177
Db      304 AGTGAAGCCGCTGATTATGTCATACATGCGCAAAATGGGATTCAGACGTGATGATCAGCCA 363
QY      178 ProLysGluLysSerLysSerAlaLysLysLysArgSerLysAlaLysGlnGln 197
Db      364 CCTAAAGAAAGAAATCCCAAGTCAAGCAAAAGAAAGAAAGCGTCCAAAGCGCAAGCA 423
QY      198 ArgGluAlaSerProValGluPheAlaIleaspProAsnGluProThyTyrCysLeuCys 217
Db      424 AGGGAAGCTTCACCTGTGATGTTGCATATGATCCTAATGACCTATGCTATG 483
QY      218 AsnGlnValSerTyrGluMetIleGlyCysAspAsnGluIysProIleGluTyr 237
Db      484 AACCAAGTCTTATGGGGAGATGATGATGATGATGATGATGATGATGATGATGATG 543
QY      238 PheHisPheSerCysValSerLeuThrTyrLysProLysGlyIysTyrPyrCysProLys 257
Db      544 TTCACCTTTCATGCTGTTTCACTTACCTATTAACCAAGGGAAGGATGGATTCACCAAG 603
QY      258 CysArgLysAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys----- 275
Db      604 TCCAGGCGGAGATATGAGAAACAAAGACAAAGC-ACGTAAGAAAGCAAAAGATGAGAA 661
QY      276 AspArgArgSerArg 280
Db      662 GATCGAAGTAAAG 676

RESULT 4
LOCUS   BE796780                      793 bp  mRNA  linear  EST 20-SEP-2000
DEFINITION 601587557F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941655 5',
ACCESSION BE796780
VERSION   BE796780.1 GI:10218080
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgabs-r@mail.nih.gov
          Tissue Procurement: DCTD/DFP
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
          DNA Sequencing by: Incyte Genomics, Inc.

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Db      184 AGCCGGCTGCTACCTGCTACGTGACAGACTACCTTGAGTGGCTGGAGTCCGTCACAC 243
QY      41 ASPMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
Db      244 GACATCGACAGCAACGTGTGTGTGCTGCGAGAGCTGGACAAATATCAAGAAAGCTTA 303
QY      61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
Db      304 AAGGAATGATGATGCTCTACGAGAAATATAGAAAGAAAGATGATTTAAACGAGAGAAA 363
QY      81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlnLeuGlnLysAspGluLys 100
Db      364 CGCTTCAGAGCTTCTCCAGAGACACTAATTAATGTAACAAATGGAGATGAGAAAA 423
QY      101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
Db      424 ATACAGATTGTTACAAATGCTCGAATTGCTGGAATGCGGCAAGACAAATGGAGTTA 483
QY      121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
Db      484 CACTCAGAGTGTTCACAGATCCTGCTGAAGTGAACGACCTCAGATTAAGCAAGATG 543
QY      141 AspSerSerGlnProGluArgSerArgArgProArgArgGlnArgThrSerGluSer 160
Db      544 GATTCACACCAACCAAAAGATCTTCAAGAGACCCCGCAGCGGACGACAGTGAAGC 603
QY      161 ArgAspLeuGlnHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
Db      604 CGTGAATTAATGTCACATGGCAATGGATGGAAGATGATGATGATGATGATGATGATGATG 663
QY      181 LysLysSerLysSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 200
Db      664 AAGAAATCCAGTCACAGCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGCT 722
QY      201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuGlnGln 219
Db      723 TCACCTGTTGAGTTGTC-ATAGATCCTAATGAACCTACATACCTTATGCAACAAG 778

RESULT 6
BM982877/c 735 bp mRNA linear EST 21-MAR-2002
LOCUS      BM982877
DEFINITION UI-CF-EN1-acs-d-05-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone
ACCESSION BM982877
VERSION    BM982877.1 GI:19606826
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 735)
            Bonaldo,M.F., Lennon,G. and Soares,M.B.
            Normalization and subtraction: two approaches to facilitate gene
            discovery
            Genome Res. 6 (9), 791-806 (1996)
JOURNAL    MEDLINE
MEDLINE    97044477
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
            cDNA library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLY-A=yes.
FEATURES
source     1..735
Location/Qualifiers

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/db_xref="taxon:9606"
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/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/Note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dr primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tag for this library is CAGCTCAGCT.
TAG_LIB=UI-CF-EN1
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS_24hr
TAG_SEQ=CAGCTCAGCT"
BASE COUNT 180 a 114 g 280 t
ORIGIN
Alignment Scores:
Pred. No.: 1,25e-77 Length: 735
Score: 1024.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.14% Indels: 0
DB: 14 Gaps: 0
US-09-513-365a-1 (1-280) x BM982877 (1-735)
QY      91 IleAsnSerGlnGlnLeuGlnLysLysIleGlnIleValThrGlnMetLeuGlnLeu 110
Db      735 ATTAATAGTCACAAATGTCGAGATGAGAAAAATACATGTTTACACAAATGCTCGAATG 676
QY      111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
Db      675 GTGGAATAATCGGCGCAAGCAAAATGAGATTACACTCAGATGTTCCAAATGCTCGAA 616
QY      131 SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerArg 150
Db      615 AGTGAACGAGCCTCAATTAAGCAAGATGATTCAGCCACAGAAAGATCTTCAAGA 556
QY      151 ArgProArgArgGlnArgThrSerGlnSerArgAspLeuGlnHisMetAlaAsnGlyIle 170
Db      555 AGACCCCGAGGAGGAGGACAGACAGTGAAGCCGATTTATGTACATGGCAATGGGATT 496
QY      171 ArgAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLys 190
Db      495 GAAGACTGTGATGATCAGCACCTTAAGAAAAAATCAAGTCACAGCAAGAAAAAGAAA 436
QY      191 ArgSerLysAlaLysGlnGlnArgGluAlaSerProValGluPheAlaIleAspProAsn 210
Db      435 CGCTCCAGGCGCAAGGAGAAAGGAGGCTTCCCTGTTGAGTTGCAATAGATCCTAAT 376
QY      211 GluProThrTyrCysLeuGlnGlnValSerTyrGlnIleGlnMetIleGlnCysAspAsn 230
Db      375 GAACCTACATCTACTGTTATGACACCAAGTGTCTTATGGGAGATGATGATGATGAT 316
QY      231 GluGlnCysProIleGluThrPheHisPheSerCysValSerLeuThrTyrLysProLys 250
Db      315 GAACAGTGTCCATTAATGATGTTTCACTTTCATGTTTCACTTACCTATTAACCAAG 256
QY      251 GlyLysTyrTyrCysProLysCysArgGluAspAsnGlnLysThrMetAspLysSerThr 270

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Db 255 GGGAAATGGTATTATCCCAAGTCAGGAGGATATGAGAAACAATGACAAAGACTACT 196
 Oy 271 GGUUThrlslyspargargserarg 280
 Db 195 GAAAAGCAAAAAGATGAGATGAGAG 166
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 LOCUS BGI184056
 DEFINITION RST2972 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.
 ACCESSION BGI184056
 VERSION BGI184056.1 GI:13705743
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 798)
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,
 E., Veloso,N., Kljka,A., Hess,J., Cochren,K., Lo,K., Offenbacher,
 J., Danzig,J. and Ducar,M.
 TITLE Creation of genome-wide protein expression libraries using random
 activation of gene expression
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
 MEDLINE 21227151
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 531.
 Location/Qualifiers
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 BASE COUNT 197 a 178 c 130 g 293 t
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 Pred. No.: 4.15e-76 Length: 798
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 Query Match: 67.96% Indels: 6
 Gaps: 0
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 Oy 82 Lcunglneuglnargalaleuileasnsrglnlueuglnargulysle 101
 Db 740 CTACAGAGCTTCTCCAGAGACCTATTAT-AGTCAAGAAATGGGAGATGAAAAAA- 683
 Oy 102 GGUUThrlslyspargargserarg 280
 Db 682 CAAATGTTCA-CAATGCTCGAATGCTGGA-AAATGGGCAAGACAAATGGAGTTTAC 625
 Oy 122 SerGlnCysPheGlnAspProAlaGluSerGlnArgAlaSerAspLysAlaLysMetAsp 141

Db 624 TCACAGTGTTCACAGATCCTGCTGAAGTGAACGAGCCCTCAGATTAAGCAAGATGAT 565
 Oy 142 SerSerGlnProGlnArgSerArgargProargglnarglnrserglnserarg 161
 Db 564 TCACAGCCACCAAGAAATATCTCAAGAAAGCCCGGAGGAGGAGCAAGTGAAGCCGT 505
 Oy 162 AspleucysHsMetAlaAsnglylleglAspCysAspAspGlnProPolysGlnLys 181
 Db 504 GATTATGTCACATGCAAAATGGGATGGAAGACTGATGATGATGATGATGATGATGATGAT 445
 Oy 182 LysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGlnArgLysAlaSer 201
 Db 444 AAATCCAGTCACCAAGAAAGAAAGAAAGCCCTCCAGAGCCCAAGCAAGCAAGCAAGCTTCA 385
 Oy 202 ProValGlnPheAlaIleAspProAsnGlnProThrLysLysLysLysLysLysLysLys 221
 Db 384 CCGTGTGATTTGCAATAGATCCCAAGAAAGCTCAATACGCTTATCAACCAAGTCTCT 325
 Oy 222 TyTGlyGlnMetIleGlyCysAspAsnGlnGlnCysProIleGlnTrpPheHsPheSer 241
 Db 324 TATGGGAGATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265
 Oy 242 CysValSerLeuThrTyLysProLysGlyLysTrpTyrcysProLysCysArgGlyAsp 261
 Db 264 TGCTTTCACCTTACTTAAACCAAGGAGAAATGATGATGATGATGATGATGATGATGATGAT 205
 Oy 262 AsnGlnLysThrMetAspLysSerThrGlnLysThrLysLysLysLysLysLysLysLys 280
 Db 204 AATGAGAAACAAATGACAAAGATGATGAAAGCAAAAGATGATGATGATGATGATGATGATGAT 148
 RESULT 8
 BM719460 664 bp MRNA linear EST 01-MAR-2002
 LOCUS BM719460
 DEFINITION UT-E-EJ1-ajf-g-22-0-UT-1 UT-E-EJ1 Homo sapiens cdna clone
 UT-E-EJ1-ajf-g-22-0-UT 5', mRNA sequence.
 VERSION BM719460.1 GI:19038113
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 664)
 AUTHORS Bonaldo,M.F., Denon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clones Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..664
 /organism="Homo sapiens"
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 /clone_lib="UT-E-EJ1"
 /tissue_type="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11022 row: e column: 10
High quality sequence stop: 722.

FEATURES
source
Location/Qualifiers
1. 891
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/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo df. Average insert size 1.5 kb. Library prepared by Life Technologies."

BASE COUNT 237 a 199 c 149 g 306 t

ORIGIN

Alignment Scores:
Pred. No.: 3,58e-67 Length: 891
Score: 902.00 Matches: 192
Percent Similarity: 85.11% Conservative: 8
Best Local Similarity: 81.70% Mismatches: 25
Query Match: 60.90% Indels: 11
DB: 13 Gaps: 2

US-09-513-365a-1 (1-280) x BI091047 (1-891)

OY 56 TrrGlnGlnThrLeuLysGluLeuAspAspValTrrGlnLysTrrLysLys---GluAs 74
DB 829 TTTCAGGAACGTCGTAATGAAATTCGATTCGATGATTAATAATGATAGACA 770
OY 74 PAsp-LeuAsnGlnLysArg-----LeuGlnGlnLeuLeuGlnArgAla-Leu 90
DB 769 TGAATGTTAAACCCAGAGAGAGAGCGTTCACAGCCAGTCCTTCCAGAGAGCACTTA 710
OY 91 IleAsnSerGlnLeuGlnLysArgGlnLysIleGlnIleVal-ThrGlnMetLeuGln 110
DB 709 ATTAATAGTCACAAATTTGGAGTATGATTAATACAGATTGACACTATGCTCGAAT 650
OY 110 UValGluAsnArgAlaArgGlnMetGlnLeuHisSerGlnCysPheGlnAspPro-Ala 130
DB 649 GGTGGTAAATCGGCA-AGACATATGAGATTACACTCACAGTGTTCACAGATCCTGCTG 591
OY 130 lUsSerGlnArgAlaSerAspLysAlaLysMet-AspSerSerGlnProGlnArgSerSer 149
DB 590 AAAGTACAGAGCTCAGATTAAGCAAAAGTGGGATTCACGCCACAGAAATCTTCA 531
OY 150 ArgArgProArgArgGlnArgThrSerGlnSerArgAspLeuGlnLysHisMetAlaAsnGly 169
DB 530 AGAAGACCCGCGAGCGAGCGACAGTGAAGCCGCGATTTATGTCACATGCGCAATGGG 471
OY 170 lIleGlnAspCysAspAspGlnProProLysGlnLysLysSerLysSerAlaLysLys 189
DB 470 ATTGAAGACTGATATGATGACCCACTAAAGAAAGAAACCAAGTACAGCAAGAAAG 411
OY 190 LysArgSerLysAlaLysGlnGlnArgGlnAlaLysSerProValGlnPheAlaIleAspPro 209
DB 410 AAACGCTCCAGGCCAAGCAGAGAAAGGAAAGCTTCACCTTTAGAGTTTGCATAAGATCT 351
OY 210 AsnGlnProThrTrrCysLeuGlnValSerTrrGlnLysLysMetIleGlnCysAsp 229
DB 350 AATGAACCTACATAGCTTATGACCAACAGTGTCTTATGGGAGATGATGATGAGAC 291
OY 230 AsnGlnGlnCysProIleGlnTrrPheHisPheSerCysValSerLeuThrTrrLysPro 249

DB 290 ACTGAACACTGTCACATTAAGTTCACCTTTCATGTCATGTCACCTAATAACCA 231
OY 250 LysGlyLysTrrPrrCysProLysCysArgGlyAspAsnGlnLysThrIleLysSer 269
DB 230 AAGGGAAATGATGATTCGCCAAAGTCAGAGGAGATTAATGAAACAAATGACCAAAAT 171
OY 270 ThrGlnLysThrLysLysAspArgSerArg 280
DB 170 ACTGAAGACAAACAAAGATGATGATGAGAG 138

RESULT 12
BF114684
LOCUS BF114684 541 bp mRNA linear EST 24-OCT-2000
DEFINITION 756608.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3391406.3 similar to TR-095698 095698 INCLIP., mRNA
sequence.
ACCESSION BF114684 GI:10984171
VERSION BF114684.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
CONTACT Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Glibco
High quality sequence stop: 459.

FEATURES
source
Location/Qualifiers
1. 541
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/clone_1lb="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773P-Pac (Pharmacia) with a modified polylinker; Site: 1; Not I; Site: 2; Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneids: Soares NBHP pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HF-9W pool 1: 758280-760583, 772104-774407 Soares NBHP pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHP pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 178 a 113 c 145 g 105 t

ORIGIN

Alignment Scores:
Pred. No.: 5.98e-67 Length: 541
Score: 897.00 Matches: 175
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.43% Mismatches: 0
Query Match: 60.57% Indels: 0
DB: 12 Gaps: 0

US-09-513-365a-1 (1-280) x BF114684 (1-541)

OY 1 MetLeuGlyGlnGlnGlnGlnLysSerSerAlaLeuLeuThrGlyGlyArg 20
|||||

```

Db 14 ATGTTAGGAGCAGCAGCAGCAACTGTACTCTGCGCTGCCATCTGACCGGGAGCGG 73
Oy 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
Db 74 AGCCGGCTGCTCAGCTCTAGTGTGAGAGCTACCTTGAAGTGTGGAGTGTGCTGCCAC 133
Oy 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
Db 134 GACATGACAGAGAAACGCTGCTGCTCGAGAGCTGACACAAATATTCAGAAACGTTA 193
Oy 61 LysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
Db 194 AAGGAATTCATGATGCTCTAGCAAAATATTAAGAAAGATGATTTAAACCAAGAA 253
Oy 81 ArgLeuGlnGlnLeuGlnArgAlaLeuLeuLeuSerGlnGlnGlnGlnGlnGlnGln 100
Db 254 CGTTTACAGCAGCTTCTCCAGAGAGCACTAATTATATGTCAGAAATGGGAGAGAA 313
Oy 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
Db 314 ATACAGATTGTATACAAATGCTCGAATGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 373
Oy 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
Db 374 CACTCAGAGTGTTCACAAAGATCCTGCTGAAAGTGAAGAGAGCTCAGATTAAGCAAA 433
Oy 141 AspSerGlnProGluArgSerSerArgArgProArgProArgGlnArgThrSerGluSer 160
Db 434 GATTCCAGCCACAGAAAGATCTTCAAGAGACCCGAGCGAGCGAGCGAGCAAGTGAAGC 493
Oy 161 ArgAspLeuCysHisMetAlaAsnGlyIleGlnAspCysAspAspGln 176
Db 494 CGTATTTATGTCTCATGCGCAATGGGATTTGAAGACGTGATGATCAG 541

RESULT 13
AV647917 679 bp mRNA linear EST 15-JAN-2002
LOCUS AV647917 GLOC Homo sapiens cDNA clone GLOCBD03 3', mRNA sequence.
DEFINITION AV647917
ACCESSION AV647917
VERSION AV647917.1 GI:9868931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 679)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
CONTACT: Zeguang Han
JOURNAL MEDLINE Chinese National Human Genome Center at Shanghai
COMMENT 351 Guo Shoujing Road, Zhanjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
SOURCE
1. 679
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLOCBD03"
/clone_lib="GLOC"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

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BASE COUNT 199 a 151 c 206 g 116 t 7 others
ORIGIN
Alignment Scores:
Pred. No.: 3,55e-66 Length: 679
Score: 889.00 Matches: 174
Percent Similarity: 95.19% Conservative: 4
Best Local Similarity: 93.05% Mismatches: 9
Query Match: 60.03% Indels: 10
Gaps: 0
US-09-513-365A-1 (1-280) x AV647917 (1-679)

Oy 1 MetLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20
Db 117 ATGTTAGGAGCAGCAGCAGCAACTGTACTCTGCGCTGCCATCTGACCGGGAGCGG 176
Oy 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
Db 177 AGCCGGCTGCTCAGCTCTAGTGTGAGAGCTACCTTGAAGTGTGGAGTGTGCTGCCAC 236
Oy 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
Db 237 GACATGACAGAGAAACGCTGCTGCTCGAGAGCTGACCAAAATATTCAGAAACGTTA 296
Oy 61 LysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
Db 297 AAGGAATTCATGATGCTCTAGCAAAATATTAAGAAAGATGATTTAAACCAAGAA 356
Oy 81 ArgLeuGlnGlnLeuGlnArgAlaLeuLeuLeuSerGlnGlnGlnGlnGlnGlnGln 100
Db 357 CGTTTACAGCAGCTTCTCCAGAGAGCACTAATTATATGTCAGAAATGGGAGAGAA 416
Oy 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
Db 417 ATACAGATTGTATACAAATGCTCGAATGTGTTGTTGTTGTTGTTGTTGTTGTTG 476
Oy 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
Db 477 CACTCAGAGTGTTCACAAAGATCCTGCTGAAAGTGAAGAGAGCTCAGATTAAGCAAA 536
Oy 141 AspSerGlnProGluArgSerSerArgArgProArgProArgGlnArgThrSerGluSer 160
Db 537 GATTCCAGCCACAGAAAGATCTTCAAGAGACCCGAGCGAGCGAGCGAGCAAGTGAAGC 596
Oy 161 ArgAspLeuCysHisMetAlaAsnGlyIleGlnAspCysAspAspGlnProLysGlu 180
Db 597 CGTATTTATGTCTCATGCGCAATGGGATTTGAAGACGTGATGATCAGCAGCTTAAGAA 656
Oy 181 LysLysSerLysSerAlaLys 187
Db 657 AAGAAATTCACAGTCAAGCAAG 677

RESULT 14
BE839427/c 564 bp mRNA linear EST 22-SEP-2000
LOCUS BE839427 RC3-FN0143-190700-022-d12 FN0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BE839427
ACCESSION BE839427
VERSION BE839427.1 GI:10271805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 564)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

```


BASE COUNT 95 a 135 c 117 g 191 t
ORIGIN

Alignment Scores:

Pred. No.: 5.38e-65 Length: 538
Score: 874.00 Matches: 169
Percent Similarity: 98.29% Conservative: 3
Best Local Similarity: 96.57% Mismatches: 3
Query Match: 59.01% Indels: 0
DB: 12 Gaps: 0

US-09-513-365A-1 (1-280) x BF523624 (1-538)

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OY      17  ThrGlyGluArgSerArgLeuLeuThrcyTyryValGlnAspTyrLeuGluCysValGlu 36
          |||
DB      536  ACCGGAGAGCGGAGCGGCTGCTCAGCTGCTAGCTGAGAGACTGCTGAGTGTGGAG 477
OY      37  SerLeuProHIsAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyr 56
          |||
DB      476  TCGCTGCCCCAGACATGACAGAGAACCTGTCGGTGGCTGCGGAGCTGACACACAATAC 417
OY      57  GlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysGluAspAspLeu 76
          |||
DB      416  CAAGAACTTAAAGGAATGATGATGCTATGAAAAATATAGAAAGAAAGATGATCA 357
OY      77  AsnGluLysArgLeuGlnGlnLeuGlnArgAlaLeuIleAsnSerGlnGluLeu 96
          |||
DB      356  AACCGAAGAAAGCGCTACAGCAGCATCTCCAGAGAGCATTAATCAATAGCCAAAGATTG 297
OY      97  GlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArg 116
          |||
DB      296  GGAGATGAAGAAAGATTGATGTCACACAGATGCTGGAATGTTGTTGAAAACCGAGCCAGA 237
OY      117  GlnMetGluLeuHIsSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 136
          |||
DB      236  CAAATGAGCTGCATTCACAGTGTTCACAGATCCTGCTGAAGTGAGCGGGCTCAGAC 177
OY      137  LysAlaLysMetAspSerSerGlnProGluArgSerArgProArgArgGlnArg 156
          |||
DB      176  AAATCCAGATGATTCAGTCACAGACCGAAAGATCTCCAGAAAGACTCGAAGAGACAGCGG 117
OY      157  ThrSerGluSerArgAspLeuCysHIsMetAlaAsnGlyIleGluAspCysAspAspGln 176
          |||
DB      116  ACCAGTGAGAGCCCGTATTAATGTCATGACAAACGGGATTGATGACTGCGATGATCAG 57
OY      177  ProProLysGluLysLysSerLysSerAlaLysLysLysArg 191
          |||
DB      56  CCACCGAAGAAAGAAATCCAAATCCGCAAAAAAAAAAAAAA 12

```

Search completed: June 20, 2003, 03:50:01
Job time : 1433 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: June 20, 2003, 01:27:39 ; Search time 241 Seconds

(without alignments)
2616.430 Million cell updates/sec

Title: US-09-513-365a-1
1481
Sequence: 1 MGGGQQQQLXSAAALLTGER.....DNEKTMKSTRETKKDRSR 280

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame-p2n.model -DEV=xlp
-O=/cgn2_1/USPRO.spool/US09513365/unal_16062003_124742_16434/app_query.fasta.1.455
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomum2 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09513365 -GCGN_1.1_366 -tunat_16062003_124742_16434 -NCP0=6 -ICP0=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_101002: *
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1481	100.0	840	20 AAZ08595	Human INGL1, encodi
2	1481	100.0	1078	20 AAZ08596	Human INGL1, encodi
3	1481	100.0	1080	22 AAD12783	Tumour suppressor
4	1345	90.8	1153	21 AAZ47473	Human tumour suppressor
5	874.5	59.0	2817	21 AAAS3790	Murine p37ING1 cod
6	853.5	57.6	911	21 AAAS3792	Human p37ING1 codi
7	853.5	57.6	1533	22 AAH28478	Nucleotide sequenc
8	853.5	57.6	2897	24 ABK66977	Human inhibitor of
9	745	50.3	1835	21 AAAS3789	Murine Ingt common
10	728	49.2	1143	22 AAH28479	Nucleotide sequenc
11	728	49.2	1902	18 AAV62285	Tumour suppressor
12	728	49.2	1902	19 AAV62285	Partial INGI parti
13	728	49.2	2061	18 AAT69652	Tumour suppressor
14	728	49.2	2061	19 AAV62292	Human INGI full-le
15	728	49.2	2061	19 AAX28688	Nucleotide sequenc
16	728	49.2	2886	24 ABK66976	Human inhibitor of
17	728	49.2	8487	22 AAL37089	Human musculoskele
18	604	40.8	742	22 AAH28480	Nucleotide sequenc
19	602	40.6	857	22 AAH28481	Nucleotide sequenc
20	572	38.6	346	21 AAC28459	Human secreted pro
21	480	32.4	693	24 ABQ50058	Oligonucleotide fo
22	480	32.4	693	24 ABQ50059	Oligonucleotide fo
23	466	31.5	693	24 ABQ50060	Oligonucleotide fo
24	466	31.5	693	24 ABQ50061	Oligonucleotide fo
25	455	30.7	1705	22 AAK51611	Human polynucleoti
26	447	30.2	1772	23 AB12805	Drosophila melanog
27	447	30.2	1781	21 AAAS3979	p33 tumour suppress
28	446.5	30.1	1465	21 AAAS1508	cDNA encoding a hu
29	446.5	30.1	1611	22 AAQ09175	Human tumour suppressor
30	446.5	30.1	1611	22 AAQ09175	Human polynucleoti
31	436.5	29.5	987	23 AB15055	Drosophila melanog
32	437.5	29.2	1365	24 AB15055	Human tumour suppressor
33	437.5	28.9	1108	22 AAF90395	Cell cycle protein
34	424.5	28.7	958	22 AAF90402	Cell cycle protein
35	406	27.4	1465	22 AAK52101	Human polynucleoti
36	400	27.0	699	21 AAA27422	Human polynucleoti
37	396.5	26.8	678	21 AAA27423	Human polynucleoti
38	392.5	26.5	807	22 AAF90400	Cell cycle protein
39	392.5	26.5	807	22 AAF90401	Cell cycle protein
40	387.5	26.2	3914	23 AB112804	Drosophila melanog
41	384.5	26.0	958	22 AAF90403	Cell cycle protein
42	362	24.4	683	24 ABQ47310	Oligonucleotide fo
43	362	24.4	683	24 ABQ47311	Oligonucleotide fo
44	359	24.2	1807	22 AAD12782	cDNA encoding huma
45	359	24.2	1864	22 AA158548	Human polynucleoti

ALIGNMENTS

RESULT 1
AAZ08595
ID: AAZ08595 standard; cDNA: 840 BP.

AAZ08595;
18-OCT-1999 (first entry)

Human INGL1 encoding cDNA.

Human: TSC403; INGL1; diagnosis; lung cancer; cell cycle; regulation;
cell proliferation; cell aging; apoptosis; tumour suppressor; ss.

Homo sapiens.

Key Location/Qualifiers
1..840
/*tag= a

Db 752 TCTTATGGGAGATGATAGGATGTGACCAATGACAGTGTCCAATTGAATGGTTTCACTTT 81

QY 1 Metleuglynglnglnglnglnleutyrserseylaalaaleuleuthrtylglylurg 20
Db 68 ATGTTAGGGGAGCAGCAGCACCACTGCTGCTGGCTGCCTCCATGCCGGGAGCG 127

OY		21	SerArgLeuIeuThcCysTyrValGlnAspTyrLengLucyValGluSerLeuProHis	40
Db		128	AGCCGGCTGCACCTCGCTACGTGCAGAGACTACTTGAGTCGCGTGGATGCCGCCAC	187
OY		41	AspMetGlnArjAsnValSerValLeuArjGluLeuAspAsnLysTyrGlnIuThrLeu	60
Db		188	GACATGCAAGNGAAGACTGCTCTGTGGCCAGAGACTGGACAACAATATCAAGAAGCTTA	247
OY		61	LysGluIlleAspAspValTyrGluTyrLysLysGluAspAspLeuAsngInLysLys	80
Db		248	AAGGAATTGATGATGCTTACGAAAATATATAAGAAAGATCATTTAAACCAGAGAAA	307
OY		81	ArgLeugIngluLeuLeugInArjAlaLeuIlleAsnSerGlngluLeugLysAspgLuLys	100
Db		308	CGTCTACAGCACCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATGGGAGATGAAAA	367
OY		101	IleGlnIlleValThrGlnMetLeugLuleuValGluAsnArjAlaarGlnMetGluLeu	120
Db		368	ATACAGATTGTATCACAAAATGCTCGAATTGGTGAAAATCGGGCAAGACAAATGGAGTTA	427
OY		121	HISserGlnCysPheGlnAspProAlaGluSerGlnArjAlaSerAspLysAlaLysMet	140
Db		428	CACCTACAGATGTTTTCCAATCCTCGTGAAGTAGAAGAGAGCCCTCAGATTAAAGCAAGATG	487
OY		141	AspSerSerGlnProGluArjSerSerArjArjProArjArgGlnArjThrSerGluSer	160
Db		488	GATTCACAGCAACACGAAAAGATCTTCAAGAAAGCCCCGCGCAGCGAGCAGATGAAAGC	547
OY		161	ArgAspLeuCysHISmetAlaAsngLylleGluAspCysAspAspgInProPolysGlu	180
Db		548	CGTGATTATATGTCACATGCGCAATGGGATTGAAGAGCTGTGATGATCAGCCACCTAAAGAA	607
OY		181	LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlngluArjGluAla	200
Db		608	AAGAAATCCAAAGTGCAGCAAAGAAAAGAAACGGCTCCAAAGGCCAAGCAGAAAGGAAGCT	667
OY		201	SerProValGluPheAlaIlleAspProAsngInuProThrTyrCysLeuCySaasngInval	220
Db		668	TCACTGTTGATTTGCAATAGTACTTAATGAACCTPAACATCGCTTATGCAACCAAGTG.	727
OY		221	SerTyrGlnGluMetIlleGlyCysAspAsngInuGlnCysProIllegluTrpPheHisPhe	240
Db		728	TCTTATGGGGAGATGATAGATGTGACAAATGAACAGTGTCCANTGATGTGTTCACTTT	787
OY		241	SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArjGly	260
Db		788	TCATGTGTTTCTACTTACCTATAAACCAAGGGGAAATGGATTTGCCCAAAAGTSCAGGGGA	847
OY		261	ASPasnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArjArgSerArg	280
Db		848	GATATATGAGAAAACAATGACAAAAGTACTGAAAAACAAAAAAGATAGAACATGCAGG	907
RESULT 4				
ID	AAZ47473		standard; cDNA; 1153 BP.	
XX	AAZ47473;			
AC	AAZ47473;			
XX	14-MAR-2000	(first entry)		
DE			Human tumour suppressor (TUSUP) nucleotide sequence.	
KW			Tumour suppressor protein; TUSUP; human; cancer; treat; prevent; reproductive tract; gastrointestinal tract; immune system; ss.	
XX				
OS			Homo sapiens.	
XX				
FH	Key	Location/Qualifiers		
FT	CDS	277..999		
FT		/tag= a		
FT		/product= TUSUP		
XX		/note= "Tumour suppressor protein"		

PN		MO9961612-A1.	
PD	02-DEC-1999.		
XX			
XX	20-MAY-1999;	99WO-US11136.	
PF			
XX			
PR	28-MAY-1998;	98US-0086359.	
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
P1	Tang YT, Corley NC, Patterson C;		
DR	WPI; 2000-062711/05.		
DR	P-PSDB; AAY52199.		
XX			
PT	New human tumour suppressor protein for treating cancer, particularly of		
FT	reproductive and gastrointestinal tracts or immune system .		
XX			
PS	Claim 7; Fig 1; 71pp; English.		
XX			
CC	This sequence encodes the human tumour suppressor (TUSUP) protein. The		
CC	TUSUP sequence was identified from a human lung cDNA library. The proteol-		
CC	is 240 amino acids in length and has one potential CAMP and GMP		
CC	dependent protein kinase phosphorylation site, nine potential protein		
CC	kinase C phosphorylation sites, five potential casein kinase		
CC	phosphorylation sites, and one potential tyrosine kinase phosphorylation		
CC	site. TUSUP has structural and chemical similarity to p33. TUSUP can be		
CC	used to treat or prevent cancer, particularly of the reproductive or		
CC	gastrointestinal tracts or of the immune system. Agonists of the TUSUP		
CC	protein can be used to raise TUSUP specific antibodies and to screen for		
CC	specific binding agents and potential therapeutic agents. The TUSUP		
CC	nucleotide sequence can be used in gene therapy and as a source of		
CC	diagnostic probes and primers.		
SO	Sequence 1153 BP; 367 A; 215 C; 285 G; 265 T; 21 other;		
	Alignment Scores:		
	Pred. No.:	1,77e-119	Length: 1153
	Score:	1345.00	Matches: 270
	Percent Similarity:	82.12%	Conservative: 1
	Best Local Similarity:	81.82%	Mismatches: 9
	Query Match:	90.82%	Indels: 52
		Gaps: 1	
US-09-513-365A-1 (1-280) x AA47473 (1-1153)			
OY	1 MetLeuNGlNGlnGlnGlnGlnLeuTYSerSerAlaAlaLeuThrGlyGluArg 20		
Db			
	9 ATGTAGACNNNNNNNNNNNNNNNNNNCTCGCGCTGGCGCTTCGACCGGGAGCGG 68		
OY	21 SerArgLeuLeuThrCysTyrrValAlGlnAspTYrLeuGluCysValGlnSerLeuProHis 40		
Db			
	69 AC-CGGCTGCTCACCTGCATCACTGACGGAGACTTGATGGTGGAGTGCCTGCCACC 127		
OY	41 AspMetGlnTrgsAnvalSerValLeuArgGlnLeuAspAsnLysTYrGln----- 57		
Db			
	128 GACATGACAGAGAAGAACTGTCTGTGCTGCAGA-CTGGACACAATAATATCAAGTCCGGGCC 186		
OY	57 ----- 57		
Db	187 TGTGCGGGCGCTTTGGTTCGGCCCCAGCGAGTCCGAATCGGGATTTCACAGATTTTYG 248		
OY	57 ----- 57		
Db	247 CGGTGATGTTTTCCAACCTCTTTTCCAGTCATGATGATCAGAGCGCGATCAGCAGCTCGGA 306		
OY	58 -----GluThrLeuLysGlnIleAspAspValTYrGlnLysTYr 70		
Db	307 CCGTCGGGATTCCTGGCTCCGCAACAGTAAGAAATGATGATGATGATGATGATGATGATGAT 366		
OY	71 LysLysGlnAspAspLeuAnsglnLysLysValArgLeuGlnLeuLeuGlnArgAlaLeu 90		
Db	367 AACAAAGAAAGATATTTAAACCAAGAAAGAACTCTACAGCAAGCTTCTCCAGAGAGCACTA 426		

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OY 91 ILeasnsrerglnluileuglyaspulubstlleglnilevalthrnglnmetleugluene 110
DB 427 ATTTAATGTCAGAAATTGGGAGATGAAATAATACAGATGTTACACAAATGCTCGAATTG 486
OY 111 Valgluasnargalaarglnmetglubehisrerglnscynsphegnasprralaglu 130
DB 487 GTGGAAATCGGGCAGACAAATGATGATTACACACAGTGTTCACAAATGCTCGTAA 546
OY 131 Sercluaralaseraplysalalysmetasrserglnprogluarargserarg 150
DB 547 AGTCAGAGAGCTCAGATTAAGCAAGATGATTCAGCCAGCAAGAAAGATCTTCAAGA 606
OY 151 Arproararglnarglnthrsergluserargapleucyshtmetalaasglyle 170
DB 607 AGACCCGCGAGCGAGCGAGCAGTGAAGCCGTAATTTATGTCACATGCGAAATGGGATT 666
OY 171 GluaspCysaspaprglnproprolysgluylslysserlysserlalyalslyls 190
DB 667 GAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCAGACGCAAGAAAGAA 726
OY 191 Argserlysalalysglnluargluaserprovalgluphealialasprrasn 210
DB 727 CGCTCCAGGCGAGGAGGAAAGGAAAGCTTCACTGTGATTGCAATGATCTTAAT 786
OY 211 Gluprothrrtyrcysleucysasnlnvalserlyrglylmetileglycysaspasn 230
DB 787 GAACCTACATACCTCTTATGCAACCAAGTCTTATGGGAGATGATGATGATGATGAT 846
OY 231 GluInCysprolelguttrpPheHisPheSerCysValSerLeuthrrtyrlysp 250
DB 847 GAACAGTGTCCAAATGGAATGTTTCACTTTTCATGTGTTTCACTTACTTAAACCAAG 906
OY 251 Glylystrprrtyrcysprolyscysarglyaspasnlnlystnmetaspyserrthr 270
DB 907 GGGGAAATGATTTCCCAAAAGTCAGAGGAGATATATGAAACAAATGAGACAAAGTACT 966
OY 271 Gluylstrlylslasparargserarg 280
DB 967 GAAGAAGCAAAAGATAGAGATCGAGC 996

RESULT 5
AAA53790
ID AAA53790 standard; cDNA; 2817 BP.
XX
AC AAA53790;
XX
DT 19-DEC-2000 (first entry)
XX
DE Murine P37ING1 coding sequence.
XX
KW p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
KW INGI; lngl; p37ING1; p37ING1; oncogene; gene therapy; diagnosis;
KW proliferation disorder; transformation; transformed cell; mouse; ds.
XX
OS Mus musculus.
XX
FT Key Location/Qualifiers
FT CDS 847..1686
FT /tag= a
FT /product= P37ING1 polypeptide
XX
PN WO200046370-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US02959.
XX
PR 04-FEB-1999; 99US-0118941.
XX
PA (UNIT ) UNIT ILLINOIS FOUND.
XX
PI Gudkov A, Zeremski M, Gurova KV, Grigorian IA;

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XX WPI: 2000-491278/43.
DR P-PSDB: AAY97242.
XX
PT Detecting nucleic acid encoding exon 1b of lngl, useful for diagnosing
PT and treating cancer, comprises contacting sample with isolated nucleic
PT acid comprising sequence of exon 1b and detecting hybridized products
XX
PS Disclosure: Fig 11; 134pp; English.
XX
CC Mutations in or loss of the p53 gene occur in more than 50% of
CC human tumours and tumour cell lines, but functional inactivation of
CC the p53 pathway occurs in a much larger proportion of tumours. In
CC many cases the mechanism of functional inactivation of the p53 gene
CC remains unknown but p53 has been found to act in cooperation with
CC INGI. Functional cooperation between INGI and p53 suggested that
CC INGI encoded a tumour suppressor protein that functioned within the
CC p53 pathway. This data suggested a possible role for INGI in head
CC and neck cancers and chromosomal location of the INGI placed it
CC within a region that is frequently rearranged in head and neck
CC cancers. Large scale analysis of tumours involving INGI has not
CC revealed mutations in INGI nor significant variations in its
CC expression suggesting that INGI was not a useful gene to study in
CC cancer etiology. However, alternative initiation exons of the lngl
CC gene, each having their own promoter have been discovered.
CC Expression of one promoter (1a) produces a protein identical to
CC INGI. Expression of a second promoter (1b) produces a protein having
CC an identical C-terminal fragment to INGI but an additional 104
CC N-terminal amino acids. The newly discovered protein has been
CC designated p37ING1 (wild type: p37ING1). p37ING1 has the
CC characteristics of an oncogene. When overexpressed in cells (even
CC those expressing wild type p53) p37ING1 is able to cause
CC proliferation or transformation of those cells. Thus detecting a
CC nucleic acid encoding exon 1b of lngl by hybridisation with an
CC isolated nucleic acid having the sequence of exon 1b of lngl
CC or its antisense sequence can identify individuals expressing the
CC oncogenic form of lngl. Novel peptide sequences taken from the 104
CC N-terminal peptide of p37ING1 can also be used to raise antibodies
CC that can also be used in detection methods for the p37ING1 variant.
CC The polypeptides may be useful in gene therapy for treatment of cell
CC proliferation disorders, especially cancers and for diagnosing and
CC studying cancers.
XX
SQ Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other:
XX
Alignment Scores:
Pred. No.: 7,04e-74 Length: 2817
Score: 874.50 Matches: 165
Percent Similarity: 77.41% Conservative: 44
Best Local Similarity: 61.11% Mismatches: 50
Query Match: 59.05% Indels: 11
DB: 21 Gaps: 3
XX
US-09-513-365A-1 (1-280) x AAA53790 (1-2817)
OY 18 GlyluargserargleuLeuthrcysrtyrvalgluaspyrleugluclvasgluser 37
DB 865 GGGGAGCAGATCCACTGTGTGAC--TATGGGAGGATTAACCTGAGTCAATGACGTCA 921
OY 38 LeuproHisapmetgluarapsnvalserValleuAAGluLeuaspaslnlystysln 57
DB 922 CTGCTTTCAGACTGCAGAGACGCTCGCTGATGCGGAGATCGAGCCCAATACCAA 981
OY 58 Gluthrleuylsgluileaspaspvaltyrclutlytyrlyslglnaspaspleuasn 77
DB 982 GAGATCTCGAAGAGAGCTGAGCAGACTACTATGAGAAAGTCAACAGGAGACAGCGCACC 1041
OY 78 GlutylslyargleuglnleuLeuenglnrAlaLeuileasnsrerglnluengly 97
DB 1042 CAGAGCGCGGGTACTGCACTGCATCCAGAGGGCGCTGATCCGACGAGAGCTAGGC 1101
OY 98 AspgluylsileglnilevalthrnglnmetleugluLeuValgluasnaralargln 117

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Db 1102 GATGAGAAGATCCAGATCGTCACTGAGTGTGAGAGCCGACGACAG 1161
Qy 118 MetGlutLeuHisSerGlnCysPhe-----GlnAspProAlaGlnSerGluArgAla 134
Db 1162 GTGGACAGTCACTGAGGAGCTCTTGAAGACACACAGACATCACTGACGACTGGTGC 1221
Qy 135 SerAspLysLysMetAspSerSerGlnProGluArg----- 147
Db 1222 AGCGGACAGCGGGCGGACGACAAAGTCGAGAGTGCACATCAGCAGAGATTAACCG 1281
Qy 148 SerSerArgArgProArgArgGlnArgThrSerGlnSerArgAspLeuCysHisMetAla 167
Db 1282 AATTAACAGAGCGTCCAGAGAGCCGAAACAAATGAGAGAGAAAGCCGTCGAAATTAAT 1341
Qy 168 AsnGly11LeuLysAspCysAspAspGlnProProLysGluLysSerLysSerAlaLys 187
Db 1342 CACGACCATGATGATGACATCACCCTCAGAAAGCCCAAGAGAGAAAGAAAGAAAGCTCAAG 1401
Qy 188 LysLysLysArgSerLysLysAlaLysGlnGlnArgGlnAlaSerProValGluPheAlaIle 207
Db 1402 AAGAGAAACGCTCCAGAGCCAAAGCAGAGAGGAAACGCTCTCTCCGACCTTCCATC 1461
Qy 208 AspProAsnGlnProThrTrpCysLeuCysAsnGlnValSerTrpGlyGluMetIleGly 227
Db 1462 GACCCACAGAGCCGACGAGTCTGTGTGCAACAGGATCTCTACGGGGAGATGATGAGC 1521
Qy 228 CysAspAsnGlnLysCysProLysGlnLeuTrpPheHisPheSerCysValSerLeuThrTyr 247
Db 1522 TGTGACAGACGAGAAATGCCCCCATCGAGTGTCCACTTCTCCGCGGGGGCTCAACCAT 1581
Qy 248 LysProLysGlnLysTrpLysTrpCysProLysCysArgGlnLysAsnGlnLysLysMetAsp 267
Db 1582 AAACCAAGGAGGAGGAGTGTACTGCCCCCAAGTGCCTGGGAGGAGCGAAGACCATGAGC 1641
Qy 268 LysSerThrGlnLysThrLysLysAspArg 277
Db 1642 AAGCCCTGGAGAGATCTCAAGAAAGAGAGC 1671

RESULT 6
AAAS3792
ID AAAS3792 standard; cDNA; 911 BP.
XX
AC AAAS3792;
XX
DT 19-DEC-2000 (first entry)
XX
DE Human P37ING1 coding sequence.
XX
KW p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
KW ING1; Ing1; p37ING1; p37ING1; oncogene; gene therapy; diagnosis;
KW Proliferation disorder; transformation; transformed cell; human; ds.
OS
XX Homo sapiens.
XX
PN WO200046370-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US02959.
XX
PR 04-FEB-1999; 99US-0118941.
XX
PA (UNIT ) UNIV ILLINOIS FOUND.
XX
PI Gudkov A, Zeremski M, Gurova KV, Griorian IA;
XX
DR P-FSDB; AAY97244.
XX
PT Detecting nucleic acid encoding exon 1b of Ing1, useful for diagnosing
PT acid comprising sequence of exon 1b and detecting hybridized products
XX

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PS Disclosure; Page 122-123; 134pp; English.
XX
CC Mutations in or loss of the p53 gene occur in more than 50% of
CC human tumours and tumour cell lines, but functional inactivation of
CC the p53 pathway occurs in a much larger proportion of tumours. In
CC many cases the mechanism of functional inactivation of the p53 gene
CC remains unknown but p53 has been found to act in cooperation with
CC ING1. Functional cooperation between ING1 and p53 suggested that
CC ING1 encoded a tumour suppressor protein that functioned within the
CC p53 pathway. This data suggested a possible role for ING1 in head
CC and neck cancers and chromosomal location of the ING1 placed it
CC within a region that is frequently rearranged in head and neck
CC cancers. Large scale analysis of tumours involving ING1 has not
CC revealed mutations in ING1 nor significant variations in its
CC expression suggesting that ING1 was not a useful gene to study in
CC cancer etiology. However, alternative initiation exons of the Ing1
CC gene, each having their own promoter have been discovered.
CC Expression of one promoter (1a) produces a protein identical to
CC ING1. Expression of a second promoter (1b) produces a protein having
CC an identical C-terminal fragment to ING1 but an additional 104
CC N-terminal amino acids. The newly discovered protein has been
CC designated p37ING1 (wild type: p33ING1). p37ING1 has the
CC characteristics of an oncogene. When overexpressed in cells (even
CC those expressing wild type p53) p37ING1 is able to cause
CC proliferation or transformation of those cells. Thus detecting a
CC isolated acid encoding exon 1b of Ing1 by hybridisation with an
CC nucleic acid nucleic acid having the sequence of exon 1b of Ing1
CC or its antisense sequence can identify individuals expressing the
CC oncogenic form of Ing1. Novel peptide sequences taken from the 104
CC N-terminal peptide of p37ING1 can also be used to raise antibodies
CC that can also be used in detection methods for the p37ING1 variant.
CC The polypeptides may be useful in gene therapy for treatment of cell
CC proliferation disorders, especially cancers and for diagnosing and
CC studying cancers.
XX
SQ Sequence 911 BP; 228 A; 255 C; 305 G; 123 T; 0 other:

Alignment Scores:
Pred. No.: 1.65e-72 Length: 911
Score: 853.50 Matches: 161
Percent Similarity: 75.74% Conservative: 45
Best Local Similarity: 59.19% Mismatches: 51
Query Match: 57.63% Indels: 15
DB: Gaps: 3

US-09-513-365A-1 (1-280) x AAAS3792 (1-911)
Qy 18 GYGLuArgSerArgLeuLeuThrCysTyValGlnAspTrpLeuGluCysValGlnSer 37
Db 63 GGGGAGCAGCTCCACCTGGTGAAAC--TATGTGAGAGACTACCTGGACTCATCGAATCC 119
Qy 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTYGln 57
Db 120 CTGCTTTCGACTTGAGAGAAATGCTGCTGATGCGGAGATGACGCGGAATATACAA 179
Qy 58 GlnThrLeuLysGlnLeuLeuAspAspValTyrGlnLysTyLysGlnAspAspLeuAsn 77
Db 180 GAGATCCTGAAGAGAGTGAAGAGAGTGTACAGCGCTTCACTGCGGAGACGAGGGCGC 239
Qy 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlnGly 97
Db 240 CAGAGGCGGCGGATGCGACCTGTGTGACGCGGCGGTATCCGACCCAGGAGCTGGGC 299
Qy 98 AspGlnLysLysGlnLeuValThrGlnMetLeuGlnLeuValGlnAsnArgAlaArgGln 117
Db 300 GACGAGAGATCCAGATCGTGAAGAGATGTTGAGAGTGTGAGAAAGCCGACGCGGAG 359
Qy 118 MetGlutLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 360 GTGGACAGCCAGCTGAGGAGTGTGAGAGCCAGCAGAGAGCTGGCGACAGTGGGCAAC 419
Qy 131 -----SerGluArgAlaSerAspLysLysLysMetAspSerSerGlnPro 145

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Db 420 AGCGCAGAGTTGGCGCGACAGGCCCAATGCGATGCGGTAGCGCACTGTACAAAGCCC 479
Oy 146 GluArgSerSerArgProArgArgGlnArgThrSerGlnuserArgAspLeucylshs 165
Db 480 -----AACGACGACCGCTCACGGGCGGACGCAACGAGAACCGTGAGAACCGCTCC 533
Oy 166 MetAlaAsnGlyIleGluAspCysAspAspGlnProPolysGluLysSerLysSer 185
Db 534 AGCAACACGACGACGACGAGCGGCGCTCGGCGACACCCAGGAGAGAACAGCCAGACCC 593
Oy 186 AlalysLysLysLysArgSerLysAlaLysGlnGlnArgGlnAlaSerProValGlnPhe 205
Db 594 TCCAGAGAGAGAGAGCGCTCCCAAGCGCCAGAGCGGCGCTCCCTCCGACCTCC 653
Oy 206 AlaIleAspProAsnGlnProThrTrpCysLeucylAsnGlnValSerTyrGlyLysMet 225
Db 654 CCATCGACCCCAAGAACCCACGACTGTCTGTCAACCAAGTCTCTATGGGAGATG 713
Oy 226 IleGlyCysAspAsnGlnGlnCysProIleGlnTrpPheHisPheSerCysValSerLeu 245
Db 714 ATCGGCTCGACGACGACGAGAGTGGCCCATCGAGTGTCTCCACTTCTCGTGGCGGCTC 773
Oy 246 ThrTyrLysProLysGlyLysTyrTrpCysProLysCysArgGlyAspAsnGlnLysThr 265
Db 774 AATCATAAACCCAAAGGCGCAAGTGTACTGTCCAAAGTCCGGGGGAGAGACGAGAACCC 833
Oy 266 MetAspLysSerThrGlnLysLysThrLysLysAspArg 277
Db 834 ATGGACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 869

RESULT 7
AAH28478
ID AAH28478 standard; DNA; 1533 BP.
AC AAH28478:
XX
XX
XX 17-SEP-2001 (first entry)
DE Nucleotide sequence of a human cancer associated antigen.
XX
XX Cancer associated antigen; INGI; tumour suppressor; cancer; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 451..1290
FT
FT /*tag= a
FT /transl_except= "(pos: 817..819, aa: Val)"
FT /transl_except= "(pos: 835..837, aa: Val)"
FT /transl_except= "(pos: 853..855, aa: Asn)"
FT /transl_except= "(pos: 859..861, aa: Asp)"
FT /transl_except= "(pos: 865..867, aa: Val)"
FT /transl_except= "(pos: 874..876, aa: Ser)"
FT /product= "cancer associated antigen"

MO200147959-A2.
XX
XX 05-JUL-2001.
XX
XX 29-NOV-2000; 2000WO-US42334.
XX
XX 30-NOV-1999; 99US-0451739.
PR 24-OCT-2000; 2000US-0602362.
XX
XX (LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
XX Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX
XX WPI: 2001-441706/47.
XX
XX P-PSDB: AAB84698.

PI Isolated cancer associated nucleic acid molecule identified by SEREX
PI (serological identification of antigens by recombinant expression
PI cloning) technique, useful in nucleic acid based therapies to treat
PI cancer -
XX
XX Claim 1; Page 43-44; 62pp; English.
XX
XX The present sequence encodes a human cancer associated antigen.
CC The sequence is a variant of the INGI gene, which is a tumour
CC suppressor gene candidate. The cancer associated antigen polynucleotides
CC and polypeptides are useful for screening for the possible presence of
CC a pathological condition in a subject such as cancer. The cancer
CC associated antigen polypeptides are useful for producing vaccines.
XX
SQ Sequence 1533 BP; 336 A; 431 C; 521 G; 244 T; 1 other;
Alignment Scores:
Pred. No.: 3,27e-72 Length: 1533
Score: 853.50 Matches: 160
Percent Similarity: 76.30% Conservative: 46
Best Local Similarity: 59.26% Mismatches: 53
Query Match: 57.63% Indels: 11
DB: 22 Gaps: 3
US-09-513-365A-1 (1-280) x AAH28478 (1-1533)
Oy 18 GlyGluArgSerArgLeuLeuThrCysTyrTyrAlaGlnAspTyrLeuGluCysValGlnSer 37
Db 469 GGGGAGCGACCTCCACCTGCTGTGAC--TATGTGGAGAGCTACTGCTGCTCCATCCAGTCC 525
Oy 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGlnLeuAspAsnLysTyrGln 57
Db 526 CTGCTTTCGACTTCAGAGAAATGCTTCGCGTGAATCGCGGAGATCGACGCGAAATACCA 585
Oy 58 GlnThrLeuLysGlnIleAspAspValTyrGlnLysLysLysGluAspAspLeuAsn 77
Db 586 GAGATCTTGAAGAGACTAGACGAGTGTGAGCGCGCTGATCCGACGAGAGCTGGCG 645
Oy 78 GlnLysLysArgGlnGlnLeuLeuGlnAlaGlnAlaLeuIleAsnSerGlnGluLeuGly 97
Db 646 CAGAGCGCGGATCTCCTCCTGTGTGAGCGCGGCTGATCCGACGAGAGCTGGCG 705
Oy 98 AspGlnLysIleGlnIleValThrGlnMetLeuGlnLeuValGlnAsnArgGlnArgGln 117
Db 706 GACGAGAAATCTCAATCTGTAGCCAGATGTGGAGCTGTGTGAGAACCGACGCGCGAG 765
Oy 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGln--SerGlnArgAlaSerAsp 136
Db 766 GTGGACAGCAGCTGAGAGCTGTTCGAGCGGACGAGAGCTGGCGGACACAGCGGCAAC 825
Oy 137 LysAlaLysMetAspSerSerGlnPro-----GlnArg 147
Db 826 AGCGGCAAGGCTGGCGGACGACGCCCAAGGCGGAGCGGCGGACGCGGCTGACCAAGCC 885
Oy 148 SerSerArgArgProArgArgGlnArgThrSerGlnuserArgAspLeucylshsMetAla 167
Db 886 AACAGCAGCGCTCAGCGGCGGACGCAACAGAGAACCGTGAGAACCGCTCCAGCAAC 945
Oy 168 AsnGlyIleGluAspCysAspAspGlnProPolysGluLysLysSerLysSerAlaLys 187
Db 946 CACGACACGACGACGCGGCGCTCGGCGACACCCAGGAGAGAGAACGCAAGACCTCCAA 1005
Oy 188 LysLysLysArgSerLysAlaLysGlnGlnArgGlnAlaSerProValGlnPheAlaIle 207
Db 1006 AAGAGAGAGCGCTCCAGAGCGGAGCGGAGAGGCGTCCCTGCGGACCTCCCAATC 1065
Oy 208 AspProAsnGlnProThrTrpCysLeucylAsnGlnValSerTyrGlyGlnMetIleGly 227
Db 1066 GACCCCAAGAGAACCCAGCTACTGTGTGCAACGAGCTCTCTATGGGAGATGATCGGC 1125
Oy 228 CysAspAsnGlnGlnCysProIleGlnTrpPheHisPheSerCysValSerLeuThrTyr 247
Db 1126 TCGGACACGACGAGTGGCCCATCGAGTGTCTCCACTTCTGCTGGTGGCGCTCAATCAT 1185


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FT      /transl_except= "(pos: 124..126, aa: Pro, Ala)"
FT      /product= "Cancer associated antigen"
XX      MO200147959-A2.
XX      05-JUL-2001.
XX      29-NOV-2000; 2000WO-US42334.
XX      30-NOV-1999; 99US-0451739.
XX      24-OCT-2000; 2000US-0602362.
XX      (LUDM-) LUDWIG INST CANCER RES.
XX      (SLOK) SLOAN KETTERING INST CANCER RES.
XX      (CORR) CORNELL RES FOUND INC.
PI      Jager D, Stockert E, Scanlan M, Knuth A, Old L, Gure A, Chen Y;
XX      WPI; 2001-441706/47.
XX      P-PSDB; AAB84697.
XX      Isolated cancer associated nucleic acid molecule identified by SEREX
XX      (serological identification of antigens by recombinant expression
XX      cloning) technique, useful in nucleic acid based therapies to treat
XX      cancer.
XX      Example 4; Page 44; 62pp; English.
XX      The present sequence encodes a human cancer associated antigen.
XX      The sequence is the wildtype of the INGI gene, which is a tumour
XX      suppressor gene candidate. The cancer associated antigen polynucleotides
XX      and polypeptides are useful for screening for the possible presence of
XX      a pathological condition in a subject such as cancer. The cancer
XX      associated antigen polypeptides are useful for producing vaccines.
XX      Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
SQ      Alignment Scores:
        Pred. No.:      2,37e-60      Length:      1143
        Score:          728.00      Matches:      136
        Percent Similarity: 74.79%      Conservative: 39
        Best Local Similarity: 58.12%      Mismatches: 45
        Query Match:      49.16%      Indels:      14
        DB:                22      Gaps:        2
US-09-513-365a-1 (1-280) x AAB28479 (1-1143)
QY      56 TyGInGluThrLeuIysGluIleAspAspValTyrGluTyrIleGluAspAsp 75
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      190 TGGAACAGATCTGTAAGAGAGCTAGACAGAGTCTGACAGCGCTTCACTCGGAGACAGAC 249
QY      76 LeuAnGlnIysIleAspArgLeuGlnGlnLeuLeuGlnIleAsnSerGlnGlu 95
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      250 GGGGCGCAGAGAGCGCGATGCTGCACTGTGTGACAGCGCGCTGATCCGACAGCAGAG 309
QY      96 LeuGlyAspGluIleGlnIleValThrGlnMetLeuGlnLeuValGluAsnArgAla 115
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      310 CTGGGGGACAGCAAGATCCAGATGAGCCAGATGATGTGAGTGAGGAGAACCCGACG 369
QY      116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      370 CGGCGAGGTGACAGCAGCTGTGAGCTGTGAGCGCAGCAGAGCTGGGCGACACAGTG 429
QY      131 -----SerGluArgAlaSerAspIleAspIleAspIleAspIleAspSer 143
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      430 GGCACAGCGCGCAAGTTGGCGCGGACAGCGCCCAATGCGATGCGGAGCGAGTCTGAC 489
QY      144 GlnProGluArgSerIleArgArgProArgArgGlnArgThrSerGlnSerArgAspLeu 163
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      490 AAGCCCG-----AAGCAGAGCGCTCAGCGGCGAGGCAACAGCAGGAGCGTGAGAAC 543
QY      164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProIleGluIleGluSer 183
DB      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB      544 GCGTCAGCAACAGCAGCAGCAGCGCGCTCGGGCACACCCCAAGAGAGAGGCC 603
QY      184 LysSerAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 1203
DB      604 AAGACCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
QY      204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuGlnValSerTyrGly 223
DB      664 GACCTCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 723
QY      224 GluMetIleGlyCysAspAsnGluGlnCysProIleIleIleIleIleIleIleIleIle 243
DB      724 GAGATGATCGGCTGCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 783
QY      244 SerLeuThrTyrIlePheGlnGluIleIleIleIleIleIleIleIleIleIleIleIle 263
DB      784 GGGCTCAATCATTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
QY      264 LysThrMetAspIleSerThrGlnIleIleIleIleIleIleIleIleIleIleIleIle 277
DB      844 AAGACCATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 885
RESULT 11
AAT69651
ID      AAT69651 standard; cDNA; 1902 BP.
XX      AC      AAT69651;
XX      DT      27-AUG-1997 (first entry)
XX      DE      Tumour suppressor gene INGI partial cDNA.
XX      KW      Tumour suppressor gene; INGI; p33ING1; breast cancer; brain cancer;
XX      diagnosis; gene therapy; ss.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      109..741
XX      FT      /tag= a
XX      PN      W09721809-A1.
XX      PD      19-JUN-1997.
XX      PE      06-DEC-1996; 96WO-CA00819.
XX      PR      15-NOV-1996; 96US-0751230.
XX      PR      08-DEC-1995; 95US-0569721.
XX      PA      (UYTE-) UNIV TECHNOLOGIES INT INC.
PI      Garkavstev I, Ribbowol K;
XX      WPI; 1997-332781/30.
XX      P-PSDB; AAW19118.
XX      Isolated tumour suppressor gene, INGI - useful to develop products
XX      for inhibiting or increasing cell proliferation, in particular for
XX      treatment or diagnosis of cancer
XX      Claim 1; Fig 2; 63pp; English.
XX      A partial cDNA clone (AAT69651), designated INGI, codes for a novel
XX      tumour suppressor protein p33ING1 (AAW19118) that is a potent
XX      inhibitor of cell growth. It was isolated by subtractive
XX      hybridisation between normal mammary and transformed epithelial
XX      cDNAs. Isolation of an antisense INGI cDNA insert that caused
XX      increased cell proliferation, and use of the insert to screen
XX      normal human fibroblast and HeLa cDNA libraries. A complete INGI
XX      sequence (AAT69652) was obt'd. by 5'RACE. INGI is localised to the
XX      19q33-34 chromosome region, to which a number of human cancers have
XX      been mapped. INGI nucleic acids can be used in the diagnosis of

```


CC breast cancer; a decreased level of INGI mRNA indicates cancerous
CC cells. They can also be used in gene therapy methods to block the
CC proliferation of cancer cells.

SO Sequence 1902 BP; 574 A; 391 C; 461 G; 476 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	1902
Score:	728.00	136
Percent Similarity:	74.79%	Conservative: 39
Best Local Similarity:	58.12%	Mismatches: 45
Query Match:	49.16%	Indels: 14
	18	Gaps: 2

US-09-513-365a-1 (1-280) x AAT69651 (1-1902)

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OY      56  TyrglIngluThrluLeuAspValTyrglTyrluTyrluAspasp 75
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Db      565  GAGATGATCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 624
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OY      264  LysThrluMetAspLysSerThrluTyrluTyrluTyrluTyrluTyrluTyrlu 277
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Db      685  AAGACATGAGCAAAAGCCCTGAGAGAAATCCAAAAAAGAGAG 726
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```

RESULT 12

AAV62285 standard; cDNA; 1902 BP.

AAV62285;

18-JAN-1999 (first entry)

Partial INGI partial cDNA sequence.

XX INGI gene; p33ING1; human; apoptosis; cell death; breast cancer;
KW brain tumour; gene therapy; tumour suppressor; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 109..741

PN MO9844102-A2.

PD 08-OCT-1998.

PF 26-MAR-1998; 98WO-CA00277.

PR 27-MAR-1997; 97US-0828158.

PA (UNITE-) UNIV TECHNOLOGIES INT INC.

PI Garkavtsev I, Helbing CC, Johnston RN, Riabowol K;

DR WPI; 1998-542700/46.

DR P-PSDB; AAW79674.

PT Modulating eukaryotic apoptosis by increasing p33ING1 activity -

PT using p33ING1 derivatives, to induce apoptosis in cancer cells, and

PT in the investigation of apoptotic pathways

Example 2; Fig 2; 66pp; English.

CC This is the nucleotide sequence of a human INGI (inhibitor of

CC growth) partial cDNA clone that codes for a p33ING1 polypeptide

CC (see AAW79674), a novel inhibitor of cell growth and a candidate

CC tumour suppressor. INGI is a new gene that is expressed in normal

CC mammary epithelial cells, but which is expressed only at lower

CC levels in several cancerous mammary epithelial cell lines and is

CC not expressed in many primary brain tumours. To isolate INGI, a

CC subtractive hybridisation of breast cancer cell line cDNAs was

CC performed with cDNA from normal mammary epithelial cells, and

CC subcloned cDNAs were cloned into retrovirus vector pINX.

CC Following passage through a packaging line, normal mouse mammary

CC epithelial cells were infected, and infected cells were injected

CC into nude mice. Putative transforming fragments from tumours were

CC isolated by PCR (see AAV62290-91) and subcloned into LNCX. An INGI

CC fragment was obtained and used to screen normal human fibroblast

CC and HeLa cell cDNA libraries. 2 Clones were sequenced to obtain

CC the partial INGI sequence. The complete cDNA sequence (see

CC AAV62292) was obtained by RACE. A claimed method to potentiate

CC apoptosis in a eukaryotic cell involves administering an active

CC p33ING1 peptide or an oligonucleotide encoding such as a peptide.

CC A claimed method for inhibiting apoptosis in a eukaryotic cell

CC involves administering an antisense oligonucleotide. Also claimed

CC are a method for determining the apoptotic characteristics of a

CC eukaryotic cell, an assay for determining the level of p33ING1

CC activity in a eukaryotic cell, and an isolated eukaryotic cell

CC substantially free of p33ING1 biological activity. The invention

CC discloses INGI derivatives or variants that may be used to induce

CC apoptosis in eukaryotic cancer cells.

SO Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 other;

Alignment Scores:

Pred. No.:	Length:	1902
Score:	728.00	136
Percent Similarity:	74.79%	Conservative: 39
Best Local Similarity:	58.12%	Mismatches: 45
Query Match:	49.16%	Indels: 14
	19	Gaps: 2

US-09-513-365a-1 (1-280) x AAV62285 (1-1902)

OY 56 TyrglIngluThrluLeuAspValTyrglTyrluTyrluAspasp 75

CC	mammary epithelial cell lines and is not expressed in many primary
CC	breast tumours. To isolate INGI, a subtractive hybridisation of
CC	mammary epithelial cells, and subtracted cDNAs were cloned into
CC	retrovirus vector pINX. Following passage through a packaging
CC	line, normal mouse mammary epithelial cells were infected, and
CC	infected cells were injected into nude mice. Putative transforming
CC	fragments from tumours were isolated by PCR (see AAV62290-91) and
CC	subcloned into INEX. An INGI fragment was obtained and used to
CC	screen normal human fibroblast and Hela cell cDNA libraries. 2
CC	Clones were sequenced to obtain a partial INGI sequence (see
CC	AAV62285). The complete cDNA sequence was then obtained by RACE. A
CC	claimed method to potentiate apoptosis in a eukaryotic cell
CC	involves administering an active p3ING1 peptide or an
CC	oligonucleotide encoding such as a peptide. A claimed method for
CC	inhibiting apoptosis in a eukaryotic cell involves administering an
CC	antisense oligonucleotide. Also claimed are a method for
CC	determining the apoptotic characteristics of a eukaryotic cell, an
CC	assay for determining the level of p3ING1 activity in a eukaryotic
CC	cell, and an isolated eukaryotic cell substantially free of p3ING1
CC	biological activity. The invention discloses INGI derivatives or
CC	variants that may be used to induce apoptosis in eukaryotic cancer
CC	cells.
XX	
SQ	Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 other:
Alignment Scores:	
Pred. No.:	5,14e-60 Length: 2061
Score:	728.00 Matches: 136
Percent Similarity:	74.79% Conservative: 39
Best Local Similarity:	58.12% Mismatches: 45
Query Match:	49.16% Indels: 14
DB:	19 Gaps: 2
US-09-513-365A-1 (1-280) x AAV62292 (1-2061)	
OY	56 TyrgIngluThleuLysSgLuLeaspAvlTYrGuLyTYrLYsGluAspasp 75
Db	190 TGGAACAGATCTGTGAAGAGCGTAGCGAGTCTTCACGGCAGAACAGAC 249
OY	76 LeuaSnGlUlylsArfLeugInglnIeuLeuInglnArGaLaLeuILeaSnSerGlnu 95
Db	250 GGSGCCGAGAAGCGGCGATGCTGCACACTGTGTGCAGCCGCGCTGATCCGCAAGCAGAG 309
OY	96 LeuGlnASpGUlysIlleGlnlleValThrImetLeuGluLeuValGLuaSnArgala 115
Db	310 CTGGGCGAGAGAAAGATCCAGATCGTGAGACCAGATGTTGAGCTGTGGAACACGCAGC 365
OY	116 ArgGlnMetGluLeuHisSerGlnCySpheGlnAspProAlaLnu----- 130
Db	370 CGGCAAGTGGACAGCCACGTGGAGGCTGTGCGAGCGCAGAGAGACTGGCGCACAGTG 429
OY	131 -----serGlnArGaLaseraPlyLSAlaLymetaSPser 143
Db	430 GGCAACAGCGGCAAGGTTGGCCGAGACAGGCCAATGGCGATGGCGTAGCGCACTGCAC 489
OY	144 GlnPrGluArgSerSerArgArProAargLnArGrThnSerGlnUserArgAspleu 163
Db	490 AACCC-----AACGCAAGGCGTTCACGGCGGACGCCAACACAGAACCGTGAGAAC 543
OY	164 CyshISmetALaSnGlyllleGluAsPCySaSPasGlnProPolYsgLUylsLysSer 183
Db	544 GCCTCCAGCAACACAGCACACGACGCGCGCTCGGGCACACCCCAAGAGAAAGAGCC 603
OY	184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluAragGluAlaSerProval 203
Db	604 AAACCTCCAAAGAAAGAAAGGCTCCAAGGCGCAAGGGGAGCGAGGCGCTCCCGCC 663
OY	204 GluPhaAlAleasProasnGlnProThrTYrcLyeuCYsaSnGlnValaSerTYrGly 223
Db	664 GACCTCCCATGCACCCCAACAACACACGTACTCTCTGTGCAAACAGGTTCTTANGG 723
OY	224 GluMeLIleGlyCySaSPasngluGlnCySProlleGluTrpPhenIsPheSerCYsaVal 243

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 20, 2003, 02:14:54 ; Search time 2153 Seconds
(without alignments)
3784.852 Million cell updates/sec

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Perfect score: 1481
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: gb.htg.*
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- 9: gb.pr.*
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- 11: gb.sts.*
- 12: gb.sy.*
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- 15: em.ba.*
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- 27: em.sts.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1481	100.0	1080	6	AX211560 Sequence
3	1481	100.0	1080	9	AF053537 Homo sapi
4	1481	100.0	1141	9	BC030128 Homo sapi
5	1478	99.8	843	9	AJ006851 Homo sapi
6	1399.5	94.5	1001	10	AF078834 Mus muscu
7	1197	80.8	974	9	HSING322 Homo sapi
8	1197	80.8	189972	2	AC107214 Homo sapi
9	1152	77.8	168245	2	AC128348 Rattus no
10	1041	70.3	1094	5	AY014017 Xenopus l
11	1008	68.1	42029	2	AC114762 Homo sapi
12	880.5	59.5	840	10	AF149820 Mus muscu
13	874.5	59.0	1584	10	BC016573 Mus muscu
14	874.5	59.0	2817	10	AF177757 Mus muscu
15	853.5	57.6	840	9	AF078835 Homo sapi
16	853.5	57.6	845	9	AF310392 Homo sapi
17	853.5	57.6	873	6	AF171884 Sequence
18	853.5	57.6	911	9	AF044076 Homo sapi
19	853.5	57.6	1533	6	AX367042 Sequence
20	853.5	57.6	1533	9	AF149721 Homo sapi
21	853.5	57.6	2444	9	AB024401 Homo sapi
22	853.5	57.6	2897	9	AF181850 Homo sapi
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26	748	50.5	166219	2	AC120896 Rattus no
27	730	49.3	1074	9	AF149722 Homo sapi
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29	728	49.2	1189	9	AF149723 Homo sapi
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32	728	49.2	1902	6	AR110646 Sequence
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ALIGNMENTS

RESULT 1

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DEFINITION Homo sapiens ING1L mRNA for ING1Lp, complete cds.
ACCESSION AB012853
VERSION   AB012853.1 GI:4115554
KEYWORDS  ING1Lp.
SOURCE    Homo sapiens fetal tissue_lib:fetal-brain cDNA to mRNA.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS   Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.
TITLE     Cloning of a novel gene (ING1L) homologous to ING1, a candidate
          tumor suppressor
JOURNAL   Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)
MEDLINE   99172097
REFERENCE 2 (bases 1 to 1078)
AUTHORS   Shimada,Y., Saito,A. and Horie,M.
TITLE     Direct Submission
JOURNAL   Submitted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical
          Co. Ltd., Otsuka GEN Research Institute, Kagasuno, Kawauchi-cho,
          Tokushima, Tokushima 771-0192, Japan
          (E-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),
          Fax:81-886-37-1035)
COMMENT   Sequence updated (17-Apr-1998).
FEATURES  Location/Qualifiers
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                RDLCHWANGIEDDDPPPKKSKSAKKRKAQERASPFVEAIDNPRTYCLCN
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                RRSR"
BASE COUNT 356 a 206 c 280 g 236 t
ORIGIN
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Pred. No.: 6.08e-113 Length: 1078
Score: 1481.00 Matches: 280
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-513-365A-1 (1-280) x AB012853 (1-1078)
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Db 92 ATGTTAGGCAGCAGCAGCAGCAACTGTACTCGTCGGCGCGCTCTCGACGGGAGCGG 151
QY 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGlnSerLeuProHis 40
Db 152 AGCCGCGTCTACCTGCTACGTCGAGGACTACTCTGAGTCGCGGAGTCGCTGCCCCAC 211
QY 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
Db 212 GACATCAGAGGAACGCTGCTGCTGCGAGAGCTGCACAAACAATATCAAGAAAGCTTA 271
QY 61 LysGluLeuAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
Db 272 AAGGAAATGATGATGCTCTACGAAATAATATAAGAAAGAGATGATTTAAACCAAGAAA 331
QY 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGluLeuGlyAspGluLys 100
Db 332 CGTCTACAGCAGCTTCTCCAGAGCAGCACTAATTAATAGTCAAGAAATGGGAGATGAAA 391
QY 101 IleGlnIleValThrGlnMetLeuLeuValGluAsnArgAlaArgGlnMetGluLeu 120
Db 392 ATACAGATGTTTACACAAATGCTCGAATGCTGGTGAATAATCGGCAACAAATGGAGTTA 451
QY 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
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QY 141 AspSerSerGlnProGluArgSerSerArgProArgArgGlnArgThrSerGluSer 160
Db 512 GATTCCAGCCCAACAGAAAGATCTTCAAGAAGACCCCGCAGGCGGACGAGTGAAGGC 571
QY 161 ArgAspLeuCysHisMetalAsnGlyIleGluAspCysAspAspGlnProProLysGlu 180
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QY 181 LysLysSerLysSerAlaLysLysLysLysLysLysLysLysLysLysGlnArgGluAla 200
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Db 692 TCACCTGTTGAGTTTGCATAGATGCTTAATGAACCTACATACACTGCTTATGACACCAAGTG 751
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QY 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrTrpTyrCysProLysCysArgGly 260
Db 812 TCATGTGTTTCACTTACCTATAACCAAGGGGAAATGGTATTGCCCAAAAGTGCAGGGGA 871
QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysLysAspArgSerArg 280
Db 872 GATATGAGAAACAATGTCACAAAGTACTGAAAGACAAACAAAAGATAGATAGATCGAGG 931
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LOCUS      1080 bp      DNA      linear      PAT 06-SEP-2001
DEFINITION Sequence 7 from Patent WO0159114.
ACCESSION AX211560
VERSION   AX211560.1 GI:15523814
KEYWORDS  human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1080)
AUTHORS   Harris,C.C. and Nagashima,M.
TITLE     Tumour suppressor gene, p47ing3
JOURNAL   Patent: WO 0159114-A 7 16-AUG-2001;
          THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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104 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
105 736 TCACCTGTTGAGTTGCAATAGATGCTTAATGAACCTACATACCTGCTTATGCAACCAAGTG 795
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107 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTTPheHisPhe 240
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110 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrCysProLysCysArgGly 260
111 856 TCATGTGTTTCACTTACCTATATAACCAAGGGAATGGTATTGCCCAAGAGTCAGGGGA 915
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118 LOCUS Homo sapiens mRNA for p32 protein. 843 bp mRNA linear PRI 06-JAN-2001
119 DEFINITION
120 ACCESSION AJ006851
121 VERSION AJ006851.1 GI:12053587
122 KEYWORDS ing2 gene; p32 protein.
123 SOURCE human.
124 ORGANISM Homo sapiens
125 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
126 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
127 1 (bases 1 to 843)
128 Cal.S., Freije,J.M. and Lopez-Otin,C.
129 ING2,a new possible gene supressor tumor
130 Unpublished
131 2 (bases 1 to 843)
132 Lopez-Otin,C.
133 Direct Submission
134 TITLE Submitted (08-JUN-1998) Lopez-Otin C.; Bioquimica y Biologia
135 JOURNAL Molecular, Universidad de Oviedo. Facultad de Medicina., C/ Julian
136 Claveria s/n., 33006, SPAIN
137 Claveria s/n., 33006, SPAIN
138 Location/Qualifiers
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154 RDLCHWANGIEDCDPPKEKSKSAKKRKAQREASPVFEAIDPNPTVCLN
155 QVSGEMIGCDNEQCPEWFHFCVSLYKPKGKNWYCKRCRGNEKTXDKTKKD
156 RRSR"
157 BASE COUNT 298 a 163 c 212 g 170 t
158 ORIGIN
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160 Alignment Scores:
161 Pred. No.: 7.87e-113 Length: 843
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168 US-09-513-365A-1 (1-280) x HSAJ6851 (1-843)

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104 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
105 61 AC CGCGGTGCTCAGCTGCTAGTGCAGGACTACCTTGAGTCGCTGGAGTGCCTGCCAC 120
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107 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60
108 121 GACATCGCAGGAGACGCTGCTGCTGCTGCGAGAGCTGGACCAACAATATCAAGAAACGTTA 180
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110 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80
111 181 AAGGAAATTCATGATGCTACGAAAAATATAAGAAAGAAAGATGATTTAAACCAAGAGAAA 240
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113 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlnLeuGlyAspGluLys 100
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116 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120
117 301 ATACAGATTGTTACACAAATGCTCGAATTTGGTGGAAATCGGGCAACACAAATGGAGTTA 360
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119 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140
120 361 CACTCACAGTGTCTCCAAAGATCCTGCTGAAAGTGAAGTGAACGAGCCTCAGATAAAGCAAGATG 420
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122 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160
123 421 GATTCACGCCAACCCAGAAAGATCTTCAAGAAAGACCCCGCAGGCGCAGGACCAAGTGAAGC 480
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125 161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProLysGlu 180
126 481 CGTGATTATGTCACATGGCAATGGGATGGAACACTGTGATGATGATGATGATGATGATGATG 540
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131 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
132 601 TCACCTGTTGAGTTGCAATAGATGCTTAATGAACCTACATACCTGCTTATGCAACCAAGTG 660
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134 221 SerTyrGlyGluMetIleGlyCysAspAsnGlnCysProIleGluTTPheHisPhe 240
135 661 TCTTATGGGGAGATGATAGTGTGACAAATGAACAGTGTCCAAATGATGATGATGATGATGATG 720
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137 241 SerCysValSerLeuThrTyrLysProLysGlyLysTyrCysProLysCysArgGly 260
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140 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
141 781 GATAATGAGAAACAATGGACAAAGTACTGAAAGACAAACAAAGGATAGATGAGGATCGAGG 840
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143 RESULT 6
144 AF078834 1001 bp mRNA linear ROD 09-SEP-2000
145 DEFINITION Mus musculus p33ING2 (Ing2) mRNA, complete cds.
146 ACCESSION AF078834
147 VERSION AF078834.1 GI:10039542
148 KEYWORDS
149 SOURCE Mus musculus.
150 ORGANISM Mus musculus
151 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
152 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
153 1 (bases 1 to 1001)
154 Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
155 Direct Submission
156 TITLE Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
157 JOURNAL National Cancer Institute, National Institutes of Health, 37
158 Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA

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	8..853	QY	240	PheSerCysValSerLeuThrTyrLysProLysGlyLysGlyLysThrTyrCysProLysCysArg	259
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US-09-513-365a-1 (1-280) x AF078834 (1-1001)					
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QY	20 ArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeu	39			
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QY	140 MetAspSerSerGlnProGluArgSerSerArgArgProArgGlnArgThrSerGlu	159			
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US-09-513-365A-1 (1-280) x HSiNG2S2 (1-974)

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QY 92 AsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuVal 111
Db 225 AATAGTCAAGATTTGGGAGATGAAAAAATACAGATTCTTACACAAATGCTCGAATGGTG 284
QY 112 GluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer 131
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QY 132 GluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerArgArg 151
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QY 192 SerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGlu 211
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QY 212 ProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlu 231
Db 585 CCTACATACCTCTATCAACCAAGTCTCTATGGGAGATGATAGGATGACAAATGAA 644
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RESULT-8

AC107214

LOCUS

DEFINITION Homo sapiens chromosome 4 clone RP11-367N14, WORKING DRAFT
 SEQUENCE, 8 unordered pieces.

ACCESSION

AC107214

VERSION AC107214.4 GI:20128734

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 189972)

Waterston,R.H.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 189972)
 Waterston,R.H.
 Direct Submission
 Submitted (16-JAN-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

3 (bases 1 to 189972)
 Waterston,R.H.
 Direct Submission
 Submitted (10-APR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT

On Apr 10, 2002 this sequence version replaced gi:18677601.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@watson.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0367N14

----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Chemistry: Dye-primer ET; 0% of reads
 Assembly: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 189941 bases at least Q40
 Consensus quality: 190973 bases at least Q30
 Consensus quality: 191699 bases at least Q20
 Insert size: 204000; agarose-fp
 Insert size: 199974; sum-of-contigs
 Quality coverage: 11.39 in Q20 bases; agarose-fp
 Quality coverage: 10.96 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 1253: gap of unknown length
 * 1353: contig of 1847 bp in length
 * 3200: gap of unknown length
 * 3300: contig of 1121 bp in length
 * 4421: gap of unknown length
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 * 5659: gap of unknown length
 * 5759: contig of 1108 bp in length
 * 6866: gap of unknown length
 * 6967: contig of 30151 bp in length
 * 37117: gap of unknown length
 * 37217: contig of 64185 bp in length
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 * 101503: 189972: contig of 88470 bp in length.

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Score: 1197.00 Matches: 231
Percent Similarity: 93.98% Conservative: 3
Best Local Similarity: 92.77% Mismatches: 9
Query Match: 80.82% Indels: 6
DB: 2 Gaps: 2

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QY 52 LeuAspAsnLysTyrglnGluThrLeuLysGluLeuAspValTyrglnLysTyrgln 71
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146702 CTT-----TTTTAGAACGTTAAAGGAATGATGCTCTACGAAATATAAG 146752

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QY 92 AsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuVal 111
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RESULT 9
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LOCUS Rattus norvegicus clone CH230-129P3, *** SEQUENCING IN PROGRESS
DEFINITION *** 50 unordered pieces.
AC128348
AC128348.1 GI:21908993
VERSION HTG; HTGS_PHASE1.
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 168245)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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Devilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczky,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
REFERENCE 2 (bases 1 to 168245)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

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TITLE
JOURNAL
AUTHORS
JOURNAL
COMMENT


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QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer 135
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QY 136 AspLysAlaLysMetAspSerSerGlnProGluArgSerArgArgProArgArgGln 155
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QY 236 GluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
Db 100701 GAGTGTGTTCACATTTTCCGCGTTTCTACCTACCTATTAACCAAGGGAATGGTATGTC 100760
QY 256 ProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys 275
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QY 276 AspArgArgSerArg 280
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RESULT 10
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LOCUS AY014017 1094 bp mRNA linear VRT 16-DEC-2001
DEFINITION Xenopus laevis p32INGL mRNA, complete cds.
ACCESSION AY014017
VERSION AY014017.1 GI:17864714
KEYWORDS
SOURCE
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    Xenopus laevis.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
    Xenopodinae; Xenopus.
  REFERENCE
    1 (bases 1 to 1094)
      Wagner,M.J., Gogela-Spehar,M., Skirrow,R.C., Johnston,R.N.,
      Riabowol,K. and Helbing,C.C.
      Expression of Novel ING Variants Is Regulated by Thyroid Hormone in
      the Xenopus laevis Tadpole
      J. Biol. Chem. 276 (50), 47013-47020 (2001)
      PUBMED 11600495
    2 (bases 1 to 1094)
      Helbing,C.C., Wagner,M.J., Gogela-Spehar,M., Skirrow,R.C.,
      Johnston,R.N. and Riabowol,K.
      Direct Submission
      Submitted (16-NOV-2000) Biochemistry and Microbiology, University
      of Victoria, P.O. Box 3055 Stn. CSC, Victoria, British Columbia V8W
      3P6, Canada
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ORIGIN
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  DB: 5 Gaps: 3
US-09-513-365A-1 (1-280) x AY014017 (1-1094)
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Db 109 ATGTTAGGGCAACAGCAGCAGCTTGCACACTACTCCCGAGGGAGCTCGCGGCG----- 159
QY 18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37
Db 160 ---GAGGACAGCAACTGTTGAGC---TATGTGGAGAGTACTCGTGGAGTCG 213
QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
Db 214 TTGCCCTTGGAAATCCAGAGGCGCTACTCTGTCGGGAGATCATAGCCAGTACCGG 273
QY 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspLeuAsn 77
Db 274 GAAGCTCTGAAGAAGTCGATGATGTTTGTGAAACCATTCAAACGAAAGTACGCTAAT 333
QY 78 GlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuIleAsnSerGlnGluLeuGly 97
Db 334 CACAAAGAGCGACTGTCAGCAGCTTCAGAGGGCCCTCATTTATGACCCAGAGCTGGC 393
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QY 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLys 137
Db 454 ATGGAATCTCTTTGCAAGGGCTTCTTTGATCAGGAAGAGAGTGCACAAAGTCTATG 513
QY 138 AlaLysMetAspSerSerGlnProGluArgSerArgArgProArgArgGlnArgThr 157
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QY 158 SerGluSerArgArgLeuCysHisMetAlaAsnGlyIleGluAspCysAspGlnPro 177
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QY 198 ArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCys 217
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QY 218 AsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlnGlnCysProLysTrp 237
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QY      278  ArgSerArg 280
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RESULT 11
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LOCUS   AC114762
DEFINITION Homo sapiens chromosome 4 clone RP11-366M5, *** SEQUENCING IN
PROGRESS ***, 26 unordered pieces.
ACCESSION AC114762
VERSION   AC114762.2 GI:19703333
KEYWORDS  HTG: HTGS_PHASE1.
SOURCE   Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42029)
AUTHORS   Waterston,R.H.
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 42029)
AUTHORS   Waterston,R.H.
JOURNAL   Direct Submission
Submitted (11-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 42029)
AUTHORS   Waterston,R.H.
JOURNAL   Direct Submission
Submitted (25-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT  On Mar 25, 2002 this sequence version replaced gi:19339148.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_LNH0366M05
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1408: contig of 1408 bp in length
* 1409
* 1508: gap of unknown length
* 1509
* 2728: contig of 1220 bp in length
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* 2828: gap of unknown length
* 2829
* 3902: contig of 1074 bp in length
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* 4003
* 5062: contig of 1060 bp in length
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* 5162: gap of unknown length
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* 6294: contig of 1132 bp in length
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* 6394: gap of unknown length
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Query Match: 68.06% Indels: 2
DB: 2 Gaps: 2

US-09-513-365A-1 (1-280) x AC114762 (1-42029)

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QY 52 LeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLys 71
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QY 92 AsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluVal 111
Db 15071 AATAGTCAAGATTTGGAGATGAAATAATACAGATTGTACAAATGCTCGAATGGTG 15012
QY 112 GluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer 131
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Db 14771 TCCAAGCCCAAGCAGGAAGGAGCTTCCACTGTTGAGTTTTCATATAGATCTTAATGAA 14712
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QY 232 GlnCysProIleGluThrPheHisPheSerCysValSerLeuThrTyr 247
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ACCESSION AF149820
VERSION AF149820.1 GI:6456561
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SOURCE Mus musculus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 840)
AUTHORS Rancourt,D. and Garkavtsev,I.
TITLE Structural organization and expression pattern of the murine INGI
gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 840)
AUTHORS Garkavtsev,I.V.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1999) Genome Therapeutics Corp., 100 Beaver St.,
Waltham, MA 02453, USA
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ORIGIN

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Query Match: 59.45% Indels: 11
DB: 10 Gaps: 3

US-09-513-365A-1 (1-280) x AF149820 (1-840)

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QY 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
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QY 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
Db 136 GAGATCTCAAGAGAGCTGGACGACTACTATGAGAGTTCAACGGGAGACAGACGCACC 195
QY 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly 97
Db 196 CAGAAGCGCGGGCTGCTGCACTGCATCCAGAGGGCCCTGATCCGACGAGGAGCTAGGC 255
QY 98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
Db 256 GATGAGAAGATCCAGATCGTGTGAGTGGTGGAGCTGGTGAGAACCCGACGACAGACAG 315


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|||||
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RESULT 14
AF177757
LOCUS
DEFINITION
Mus musculus INgl protein (Ingl) mRNA, alternatively spliced,
complete cds.
ACCESSION
AF177757
VERSION
AF177757.1 GI:6561423
KEYWORDS
Mus musculus.
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2817)
Zeremski, M., Hill, J.E., Kwek, S.S., Grigorian, I.A., Gurova, K.V.,
Garkavtsev, I.V., Diatchenko, L., Koonin, E.V. and Gudkov, A.V.
Structure and regulation of the mouse Ingl gene. Three alternative
transcripts encode two phd finger proteins that have opposite
effects on p53 function
J. Biol. Chem. 274 (45), 32172-32181 (1999)
20011419
MEDLINE
10542254
PUBMED
REFERENCE
2 (bases 1 to 2817)
Zeremski, M., Hill, J., Garkavtsev, I.V. and Diatchenko, L.
Direct Submission
Submitted (16-AUG-1999) Molecular Genetics, Univ. of Illinois at
Chicago, 900 South Ashland Ave., Chicago, IL 60607, USA
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BASE COUNT 670 a 711 c 846 g 590 t
ORIGIN

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Score: 874.50 Matches: 165
Percent Similarity: 77.41% Conservative: 44
Best Local Similarity: 61.11% Mismatches: 50

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RESULT 15
AF078835
LOCUS
DEFINITION
Homo sapiens p33ING1 (ING1) mRNA, complete cds.
ACCESSION
AF078835
VERSION
AF078835.1 GI:10039544
KEYWORDS
Homo sapiens.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 840)
REFERENCE
1 (bases 1 to 840)

```

AUTHORS

Nagashima,M., Shiseki,M., Miura,K., Hagiwara,K., Linke,S.P.,
 Pedoux,X.W., Wang,X.W., Yokota,J., Riabowol,K. and Harris,C.C.
 DNA damage-inducible gene p33ING2 negatively regulates cell
 proliferation through acetylation of p53
 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
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 MEDLINE
 11481424
 PUBMED

REFERENCE

2 (bases 1 to 840)
 Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
 Direct Submission
 TITLE
 JOURNAL
 Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
 National Cancer Institute, National Institutes of Health, 37
 Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA

FEATURES

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BASE COUNT 218 a 239 c 277 g 106 t

ORIGIN

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 Best Local Similarity: 59.26% Mismatches: 53
 Query Match: 57.63% Indels: 11
 DB: 9 Gaps: 3

US-09-513-365A-1 (1-280) x AF078835 (1-840)

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 Qy 188 LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle 207
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Job time : 2265 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 20, 2003, 02:42:14 ; Search time 68 seconds
(without alignments)
1262.787 Million cell updates/sec

Title: US-09-513-365A-1

Perfect score: 1481

Sequence: 1 MLGQQQQQLYSSAALLTGER.....DNEKTMDSKTEKTKDRRSR 280

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 16.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1481	100.0	840	US-09-601-478-6	Sequence 6, Appli
2	1481	100.0	1078	US-09-601-478-7	Sequence 7, Appli
3	1334	90.1	1154	US-09-484-970B-81	Sequence 81, Appl
4	853.5	57.6	873	US-09-006-783A-4	Sequence 4, Appli
5	728	49.2	1902	US-09-258-257-1	Sequence 1, Appli
6	728	49.2	1902	US-09-258-371-1	Sequence 1, Appli
7	728	49.2	1902	US-08-569-721A-1	Sequence 1, Appli
8	728	49.2	1902	US-08-751-230-1	Sequence 1, Appli
9	728	49.2	1902	US-09-499-082-1	Sequence 1, Appli
10	728	49.2	1902	US-09-258-372-1	Sequence 1, Appli
11	728	49.2	2061	US-09-258-371-9	Sequence 9, Appli
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13	728	49.2	2061	3	US-09-499-082-9	Sequence 9, Appli
14	728	49.2	2061	4	US-09-258-372-9	Sequence 9, Appli
15	728	49.2	2061	4	US-09-159-871-1	Sequence 1, Appli
16	722	48.8	2061	4	US-09-006-783A-2	Sequence 2, Appli
17	662	44.7	633	4	US-09-006-783A-6	Sequence 6, Appli
18	400	27.0	699	3	US-09-195-286-2	Sequence 2, Appli
19	396.5	26.8	678	3	US-09-195-286-3	Sequence 3, Appli
20	314	21.2	451	4	US-09-370-838-146	Sequence 146, App
21	172.5	11.6	8931	3	US-09-051-019-1	Sequence 1, Appli
22	127.5	8.6	1820	4	US-08-845-258-17	Sequence 17, Appl
23	127.5	8.6	1820	4	US-08-845-258-37	Sequence 37, Appl
24	127.5	8.6	1820	4	US-08-990-571-17	Sequence 17, Appl
25	127.5	8.6	1820	4	US-08-990-571-37	Sequence 37, Appl
26	127.5	8.6	1820	4	US-08-723-142A-17	Sequence 17, Appl
27	127.5	8.6	1820	4	US-08-723-142A-37	Sequence 37, Appl
28	127.5	8.6	1820	4	US-09-528-784A-17	Sequence 17, Appl
29	127.5	8.6	1820	4	US-09-528-784A-37	Sequence 37, Appl
30	127.5	8.6	2001	4	US-09-528-784A-84	Sequence 84, Appl
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34	122	8.2	8600	4	US-09-457-708-1	Sequence 1, Appli
35	120	8.1	1772	2	US-08-960-022-13	Sequence 13, Appl
36	116.5	7.9	543	6	5273901-6	Patent No. 5273901
37	116.5	7.9	9551	1	US-08-056-200-93	Sequence 93, Appl
38	116.5	7.9	9551	2	US-08-800-644-93	Sequence 93, Appl
39	115	7.8	812	4	US-08-998-416-401	Sequence 401, App
40	114	7.7	1053	5	PCT-US91-06418-2	Sequence 2, Appli
41	114	7.7	1621	2	US-08-933-750C-96	Sequence 96, Appl
42	114	7.7	1621	3	US-09-234-613-96	Sequence 96, Appl
43	113.5	7.7	6693	4	US-08-961-527-195	Sequence 195, App
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45	112.5	7.6	1864	1	US-08-454-720A-38	Sequence 38, Appl

ALIGNMENTS

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; Sequence 6, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Ostuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
; FILE REFERENCE: 060193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
US-09-601-478-6

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US-09-513-365A-1 (1-280) x US-09-601-478-6 (1-840)

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TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 7..813
US-09-006-783A-4

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US-09-513-365A-1 (1-280) x US-09-006-783A-4 (1-873)

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DB 796 ATGGACAAGCCCTGGAGAAATCCAAAAGAGAGG 831

RESULT 5

US-09-258-257-1
Sequence 1, Application US/09258257
Patent No. 5965398
GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, Igor
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 109..738
US-09-258-257-1

Alignment Scores:
Pred. No.: 1.2e-71 Length: 1902
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DB: Gaps: 2

US-09-513-365A-1 (1-280) x US-09-258-257-1 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsp 75
DB 31 TGGAAACAGATCTGAAGGAGGTAGACGAGTCTACGAGCGCTTCTAGTCGCGAGACAGAC 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
DB 91 GGGGGCCAGAACGCGCGGATGTGCTGTGTGACGCGCGCTGATCCGACCCAGAG 150
QY 96 LeuGlyAspLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
DB 151 CTGGGCGACGAGAAGATCCAGATCGTGACCGAGATGGTGAGCTGGTGAGAACCCGACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130

Db 211 CGCAGGTGGACACGCCACGTGGAGCTGTTCAGCGCGCAGGAGCTGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCACACGGCGAAGTTGGCGGAGACGCCCAATGGCGATGGCGTAGCGCATCTGAC 330
QY 144 GlnProGluArgSerSerArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACACGAAGCGCTACGCGCGCAGCGCAACACAGAGACCGGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 385 GCCTCCAGCAACCCACGACGAGCGCGCTCGGGCGACACCCCAAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 445 AAGACCTCCAGAGAGAGAGCGCTCCAGGCCAAGCGCGAGCGAGAGGCGTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 505 GACCTCCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACCAAGGTCTCTATGGG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 565 GAGATGATCGGCTGCGCAACGACGAGTGCCTCCATCGAGTGGTTCCTCTCTCGTGGGTG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 625 GGGCTCAATCAATAACCAAGGCAAGTGGTACTGTCTCCCAAGTGGCGGGGGAGAACGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGACAAAGCGCTGGAGAAATCCAAAAAGAGAGG 726

RESULT 6

US-09-258-371-1
; Sequence 1, Application US/09258371
; Patent No. 5986078
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,371
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A. 37, 047
; REGISTRATION NUMBER: 028722-144
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1902 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..741
US-09-258-371-1

Alignment Scores:

Pred. No.: 1,2e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 2 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-258-371-1 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp 75
Db 31 TGGAAACAGATCTTGAAGGAGCTAGACAGAGTGTACGAGCGCTTCAGTCGGGACACAG 90
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuIleAsnSerGlnGlu 95
Db 91 GGGCGCGAGAAGCGCGGATGCTGCACTGTGTGCGAGCGCGCTGTATCCGCGACGAGGAG 150
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluValGluAsnArgAla 115
Db 151 CTGGGCGACGAGAGATCCAGATCGTGCAGAGATGTGGAGCTGGTGGAGAACCGCGACG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 211 CGCGAGGTGGACACGCCACCTGGAGCTGTTCCAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 271 GGCACACGCGCAAGTTGGCGGACAGGCCCAATGGCGATGGGTAGCGCATCTCTAC 330
QY 144 GlnProGluArgSerSerArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 331 AAGCCC-----AACACGAAGCGCTCAGCGCGCAGCGCAACACAGAGACCGGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
Db 385 GCGTCCAGCAACCCACGACGACGCGCGCTCGGGCGACACCCCAAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 445 AAGACCTCCAGAGAGAGAGCGCTCCAAAGGCCAAGCGCGAGCGAGCGGCTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 505 GACCTCCCATCGACCCCAACGACCCACCTACTGTCTGTGCAACCAAGGTCTCTATGGG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 565 GAGATGATCGGCTGCGCAACGACGAGTGCCTCCATCGAGTGGTTCCTCTCTCGTGGGTG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 625 GGGCTCAATCAATAACCAAGGCAAGTGGTACTGTCTCCAAAGTGGCGGGGGAGAGAGGAG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 685 AAGACCATGACAAAGCGCTGGAGAAATCCAAAAAGAGAGG 726

RESULT 7

US-08-569-721a-1
; Sequence 1, Application US/08569721a
; Patent No. 6037121
; GENERAL INFORMATION:
; APPLICANT: GARKAVTSEV, Igor


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Pred. No.: 1.2e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2

US-09-513-365A-1 (1-280) x US-08-751-230-1 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAsp 75
DB 31 TGAACACATCTGAGAGAGTAGACGAGTCTACGAGCGTTCAGTCCGACAGACAG 90
QY 76 LeuAsnGlnLysLysArgLeuGlnLeuLeuArgAlaLeuLeuAsnSerGlnGlu 95
DB 91 GGGGCGCAGACGCGGGATGTGCTACTGTGTGACGCGCGTGTATCCGACGAGAG 150
QY 96 LeuGlyAspGluLysIleGlnLeuValThrGlnMetLeuLeuValGluAsnArgAla 115
DB 151 CTGGGCGCAGAGAGATCCAGATCGTGTGACCGAGATGTTGGAGTGTGGAGAACCGCAG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 211 CGGAGGTGGACAGCCAGTGTGAGGCGGCGCAGAGTGGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
DB 271 GGCAACAGCGCAAGGTGGCGGACAGGCCAATGGCGATCGGTACGCGAGTGTAC 330
QY 144 GlnProGluArgSerSerArgProArgGlnArgThrSerGluSerArgAspLeu 163
DB 331 AAGCCC-----AACAGCAAGCGCTCAGCGGCGCAGCGCAACAGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProLysGluLysSer 183
DB 385 GGTCCAGCAACACAGCAGCAGCGCGCTGGGCGACACCCCAAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
DB 445 AAGACTCCCAAGAGAGAGAGCGCTCCAGAGCGCAAGGCGGAGGAGCGTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
DB 505 GACCTCCCATCGACCCCAAGCAAGCAAGTGTGTGTGCAACAGGTCCTATGGG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisSerCysVal 243
DB 565 GAGATGATCGGTGGACACAGCAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
DB 625 GGGCTCAATCAATAAACCCCAAGGCAAGTGTGTGTGCAACAGGTCCTATGGG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
DB 685 AAGACCATGGCAAAAGCCCTGGAGAAATCCAAAAAGAGAGG 726

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RESULT 9

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US-09-499-082-1
; Sequence 1, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Caren C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA

```

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COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRAINEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741
US-09-499-082-1

Alignment Scores:
Pred. No.: 1.2e-71 Length: 1902
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 3 Gaps: 2

US-09-513-365A-1 (1-280) x US-09-499-082-1 (1-1902)

QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAsp 75
DB 31 TGAACACATCTGAGAGAGTAGACGAGTCTACGAGCGTTCAGTCCGACAGACAG 90
QY 76 LeuAsnGlnLysLysArgLeuGlnLeuLeuArgAlaLeuLeuAsnSerGlnGlu 95
DB 91 GGGGCGCAGACGCGGGATGTGCTACTGTGTGACGCGCGTGTATCCGACGAGAG 150
QY 96 LeuGlyAspGluLysIleGlnLeuValThrGlnMetLeuLeuValGluAsnArgAla 115
DB 151 CTGGGCGCAGAGAGATCCAGATCGTGTGACCGAGATGTTGGAGTGTGGAGAACCGCAG 210
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
DB 211 CGGAGGTGGACAGCCAGTGTGAGGCGGCGCAGAGTGGGCGACACAGTG 270
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
DB 271 GGCAACAGCGCAAGGTGGCGGACAGGCCAATGGCGATCGGTACGCGAGTGTAC 330
QY 144 GlnProGluArgSerSerArgProArgGlnArgThrSerGluSerArgAspLeu 163
DB 331 AAGCCC-----AACAGCAAGCGCTCAGCGGCGCAGCGCAACAGAGAACCGTGAGAAC 384
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProLysGluLysSer 183
DB 385 GGTCCAGCAACACAGCAGCAGCGCGCTGGGCGACACCCCAAGGAGAGAGGCC 444
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
DB 445 AAGACTCCCAAGAGAGAGAGCGCTCCAGAGCGCAAGGCGGAGGAGCGTCCCTGCC 504
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
DB 505 GACCTCCCATCGACCCCAAGCAAGTGTGTGTGCAACAGGTCCTATGGG 564
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisSerCysVal 243
DB 565 GAGATGATCGGTGGACACAGCAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 624
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
DB 625 GGGCTCAATCAATAAACCCCAAGGCAAGTGTGTGTGCAACAGGTCCTATGGG 684
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
DB 685 AAGACCATGGCAAAAGCCCTGGAGAAATCCAAAAAGAGAGG 726

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mool, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16...900

US-09-258-371-9
Alignment Scores:
Pred. No.: 1.35e-71
Score: 728.00
Percent Similarity: 74.79%
Best Local Similarity: 58.12%
Query Match: 49.16%
Indels: 14
Gaps: 2

US-09-513-365A-1 (1-280) x US-09-258-371-9 (1-2061)

QY 56 TyrGlnGlnThrLeuLysGluLeuAspValTyrGluLysTyrLysLysGluAsp 75
Db 190 TGGAAACAGATCCCTGAAGAGGCTAGACAGTGTACGAGCGCTTCAGTCCGAGCAGAC 249
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuLeuAsnSerGlnGlu 95
Db 250 GGGCGCAGAAAGCGCGGATCTGCTGCTGTGCGCGCGCTGATCCGCGCAGCAGGAG 309
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 310 CTGGCGCAGCAGAAAGATCCAGATCGTGAGCCAGATGTTGGAGCTGGTGGAGAACCGCAG 369
QY 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 370 CGGCAGTGGACAGCCAGCTGAGCTGTTCGAGCGCAGCAGAGCTGGCGCAGACACAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACACCGCAGAGTTGGCGCGCAGACAGCCCATGGCGATGGCGGTAGCGCATGCTGAC 489
QY 144 GlnProGluArgSerArgArgProArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACAGCAGCGCTCAGCGCGCAGCGCAACACAGAGACCGTGAGAAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysSer 183
Db 544 GCGTCCAGCAGCAGCAGCAGCGCGCGCTCGGCGCAGCAGCAGCAGAGAGAGGCC 603
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 604 AAGACCTCCAAAGAGAGAGCGCTCCAAAGCCCAAGCGCGCAGCAGAGCGCTCCCTGCC 663

QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCGAGCCCAACGACCCACGCTACTGTCTGTGCAACACCGTCTCTCTATGGG 723
QY 224 GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 724 GAGATGATCGGCTGCGACACGAGAGTGCCTCCATCGAGTGGTTCACCTTCTCTGTCGCTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCAATCAACCCCAAGGGCAAGTGGTACTGTCCCAAGTGCCTGGGGGAGAACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 885

RESULT 12

US-08-751-230-9
Sequence 9, Application US/08751230
Patent No. 6117633
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mool, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16...900

US-08-751-230-9
Alignment Scores:
Pred. No.: 1.35e-71
Score: 728.00
Percent Similarity: 74.79%
Best Local Similarity: 58.12%
Query Match: 49.16%
Indels: 14
Gaps: 2

US-09-513-365A-1 (1-280) x US-08-751-230-9 (1-2061)

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QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAspAsp 75
Db 190 TGAACACATCTGAAGGAGTAGACGAGTCTACGAGCGTTCAGTCGCGAGACAG 249
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuLeuAsnSerGlnGlu 95
Db 250 GGGCGCAGAGCGCGGATGTCACACTGTGTGACGCGCGTGTGCGAGCAGGAG 309
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 310 CTGGCGCAGAGAAGTCCAGATCGTGAGCCAGATGCTGGAGTGTGGAGAACCGCAG 369
QY 116 ArgGlnMetLysHisSerGlnCysPheGlnAspProAlaGlu 130
Db 370 CGCGAGGTGGACAGCCAGTGTGGAGTGTGGAGCGCAGCGAGTGGCGACACAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACACGCGCAAGTGTGGCGCGGACAGCCCAATGGCGATGCGGTAGCGAGTGTGAC 489
QY 144 GlnProGluArgSerArgProArgProArgProArgProArgProArgProArgProVal 163
Db 490 AAGCCC-----AACAGCAAGCGCTCAGCGCGCAGCGCAACAGCAGACCGTGAAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysSer 183
Db 544 GCGTCCAGCAACAGCAGCCAGCAGCGCGCGTGGCGGACAGCGAGGAGGAGGCGC 603
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGlnGluArgGluAlaSerProVal 203
Db 604 AAGACCTCCAGAGAGAGAGCGCTCCAGAGCGCAGCGGAGGAGGAGGAGGAGGAGG 663
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCGACCCCAAGCGCTCCAGAGCGCAGCGGAGGAGGAGGAGGAGGAGG 723
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Db 724 GAGATGATCGGTGCGACACGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCAATAAACCCAGGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGGACAAACCCCTGGAGAAATCCAAAAGAGAGG 885
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RESULT 13

US-09-499-082-9
Sequence 9, Application US/09499082
Patent No. 6143522

GENERAL INFORMATION:

APPLICANT: Helbing, Karen C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
US-09-499-082-9

Alignment Scores:
Pred. No.: 1.35e-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: Gaps: 2

US-09-513-365A-1 (1-280) x US-09-499-082-9 (1-2061)

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QY 56 TyrGlnGluThrLeuLysGluLeuAspValTyrGluLysTyrLysGluAspAsp 75
Db 190 TGAACACATCTGAAGGAGTAGACGAGTCTACGAGCGTTCAGTCGCGAGACAG 249
QY 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuArgAlaLeuLeuAsnSerGlnGlu 95
Db 250 GGGCGCAGAGCGCGGATGTCACACTGTGTGACGCGCGTGTGCGAGCAGGAG 309
QY 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 310 CTGGCGCAGAGAAGTCCAGATCGTGAGCCAGATGCTGGAGTGTGGAGAACCGCAG 369
QY 116 ArgGlnMetLysHisSerGlnCysPheGlnAspProAlaGlu 130
Db 370 CGCGAGGTGGACAGCCAGTGTGGAGTGTGGAGCGCAGCGAGTGGCGGACACAGTG 429
QY 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCACACGCGCAAGTGTGGCGCGGACAGCCCAATGGCGATGCGGTAGCGAGTGTGAC 489
QY 144 GlnProGluArgSerArgProArgProArgProArgProArgProArgProVal 163
Db 490 AAGCCC-----AACAGCAAGCGCTCAGCGCGCAGCGCAACAGCAGACCGTGAAC 543
QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysSer 183
Db 544 GCGTCCAGCAACAGCAGCCAGCAGCGCGCGTGGCGGACAGCGAGGAGGAGGAGGCGC 603
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGlnGluArgGluAlaSerProVal 203
Db 604 AAGACCTCCAGAGAGAGAGCGCTCCAGAGCGCAGCGGAGGAGGAGGAGGAGGAGG 663
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
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Db 664 GACCTCCCATCGACCCCAAGAACCCACGCTACTGTGTGCAACCAAGGCTCTCTATGGG 723
Qy 224 GluMetileGlyCysAspAsnGluInCysProIleGluThrPheHisPheSerCysVal 243
Db 724 GAGATGATCGCTCGGCAACGAGAGTGCCTCCATCGAGTGGTTCCTCTCTGTCGCTG 783
Qy 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCATRAAACCAAGGCAAGTGTGTCTCCCAAGTGCCTCGGGGAGAACGAG 843
Qy 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGACAAAGCCCTCGAGAAATCCAAAAAGAGAGG 885

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RESULT 14

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; US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..900
; US-09-258-372-9

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Alignment Scores:
Pred. No.: 1.35e-71 Length: 2061
Score: 728.00 Matches: 136
Percent Similarity: 74.79% Conservative: 39
Best Local Similarity: 58.12% Mismatches: 45
Query Match: 49.16% Indels: 14
DB: 4 Gaps: 2

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US-09-513-365A-1 (1-280), x US-09-258-372-9 (1-2061)

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Qy 56 TyrGlnGluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspasp 75
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Qy 76 LeuAsnGlnLysLysArgLeuGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
Db 250 GGGCGCAGAGAGCGCGGATGCTGCTACTGTGTGAGCGCGGCTGATCCGACGAGAG 309
Qy 96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
Db 310 CTGGCCACAGAGAGATCCAGATCTGACGAGATGTTGGAGCTGTGGAGAACCGCAG 369
Qy 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
Db 370 CGCAGGTGGACACCGACGCTGCTGAGCGCGCAGGAGCTGGGCGACACAGTG 429
Qy 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
Db 430 GGCAACACGCGCAAGGTTGGCGGACAGGCCCAATGGCGATGGCGTACGCTGTGAC 489
Qy 144 GlnProGluArgSerArgArgArgGlnArgThrSerGluSerArgAspLeu 163
Db 490 AAGCCC-----AACACGAGCGCTCAGCGCGGAGCGCAACACAGGACCGTGAGAAC 543
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Db 544 GCGTCCAGCAACACGACGACGCGCGCCCTCGGCGCACACCAAGGAGAGAGGCC 603
Qy 184 LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
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Qy 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 564 GACCTCCCATCGACCCCAACGACCCACGCTACTGTCTGTCAACACGAGTCTCTATGG 723
Qy 224 GluMetileGlyCysAspAsnGluInCysProIleGluThrPheHisPheSerCysVal 243
Db 724 GAGATGATCGGCTCGGACACGAGGAGTGCCTCCATCGAGTGGTTCCTCTCTGCGTG 783
Qy 244 SerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGGCTCAATCATRAAACCAAGGCAAGTGTGTCTCCCAAGTCCCGGGGAGAACGAG 843
Qy 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGACAAAGCCCTCGAGAAATCCAAAAAGAGAGG 885

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RESULT 15

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; US-09-159-871-1
; Sequence 1, Application US/09159871A
; Patent No. 6420136
; GENERAL INFORMATION:
; APPLICANT: RIABOWOL, Karl T.
; TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
; FILE REFERENCE: 028722-181
; CURRENT APPLICATION NUMBER: US/09/159,871A
; CURRENT FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/060,138
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: US 09/006,783
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(897)
; US-09-159-871-1

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Alignment Scores:

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DB:	4	Gaps:	2

US-09-513-365A-1 (1-280) x US-09-159-871-1 (1-2061)

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QY	: : : : : : : : :	
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76	LeuAsnGlnLysLysArgLeuGlnGlnLeuGlnArgAlaLeuLeuAsnSerGlnGlu	95
QY	: : : : : : : :	
250	GGGGCGCAGAGCGCGGATCGTCACTGTGTGCAGCGCGCTGATCCGACCGAGAG	309
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96	LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGlnLeuValGluAsnArgAla	115
QY	: : : : : : : :	
310	CTGGCGCAGCAGAGATCCAGATCGTGAAGCAGATGGTGAGCTGGTGGAGAACCCGACG	369
DB	: : : : : : : :	
116	ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu	130
QY	: : : : : : : :	
370	CGGCAGGTGGACGCCATCGTGAGCTGTTCGAGCGCGACGAGCTGGCGGCACACAGTG	429
DB	: : : : : : : :	
131	-----SerGluArgAlaSerAspLysAlaLysMetAspSerSer	143
QY	: : : : : : : :	
430	GGCAACAGCGCGAAGTTGGCGCGACAGCGCCCAATGGCGATCCGTCGTCAGTCTGAC	489
DB	: : : : : : : :	
144	GlnProGluArgSerArgArgProArgArgGlnArgThrSerGlnSerArgArgLeu	163
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490	AAGCCCC-----AACAGCAGCGCTCAGCGCGCGACGCCAACACAGAGAACCGTGAGAAC	543
DB	: : : : : : : :	
164	CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysLysSer	183
QY	: : : : : : : :	
544	GGTCCAGCAACACGACGACGCGCGCTCGGGCACACCCAGAGAGAGAGGCC	603
DB	: : : : : : : :	
184	LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal	203
QY	: : : : : : : :	
604	AAGACCTCCAAAGAGAGAGACGCGTCCAAAGCGGAAGCGGAGGAGCGCTCCCTGCG	663
DB	: : : : : : : :	
204	GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly	223
QY	: : : : : : : :	
664	GACCTCCCATCGACCCCAAGAACCCACGCTACTGTCTGTGCACACAGGTCTCCTATGG	723
DB	: : : : : : : :	
224	GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal	243
QY	: : : : : : : :	
724	GAGATGATCGCTCGCACACGACGAGTGGCCCATCGAGTGGTTCACATCTTCGTGCGGT	783
DB	: : : : : : : :	
244	SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu	263
QY	: : : : : : : :	
784	GGGCTCATATNAACCAAGGGCACTGGTACTGTGCCCAAGTCCCGGGGGAGAACGAG	843
DB	: : : : : : : :	
264	LysThrMetAspLysSerThrGluLysThrLysLysAspArg	277
QY	: : : : : : : :	
844	AAGACCATGGAACAGCGCTTGAAGAAATCCAAAGAGAGAGG	885
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Job time : 81 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 20, 2003, 03:27:49 ; Search time 160 Seconds

(without alignments)
2567.998 Million cell updates/sec

Title: US-09-513-365A-1

Perfect score: 1481

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Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09513365 -CGCN_1_1.80 -runat_16062003_124745_16556
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1481	100.0	840	12	US-10-115-899-6
2	1481	100.0	1078	12	US-10-115-899-7
3	853.5	57.6	873	9	US-09-968-653A-4
4	728	49.2	8487	10	US-09-764-877-3454

Sequence 6, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 3454, Ap

ALIGNMENTS

RESULT 1

US-10-115-899-6

; Sequence 6, Application US/10115899

; Patent No. US20020151025A1

; GENERAL INFORMATION:

; APPLICANT: Ostuka Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Human TSC403 gene and human INGL1 gene

; FILE REFERENCE: Q60193

; CURRENT APPLICATION NUMBER: US/10/115.899

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 09/601,478

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP H10-134679

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: JP H10-73234

; PRIOR FILING DATE: 1998-03-05

; PRIOR APPLICATION NUMBER: JP H10-38133

; PRIOR FILING DATE: 1998-02-03

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 840

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

Sequence 2, Appli
Sequence 6, Appli
Sequence 37033, A
Sequence 435, App
Sequence 146, App
Sequence 1178, Ap
Sequence 257, App
Sequence 16047, A
Sequence 370, App
Sequence 471, App
Sequence 142, App
Sequence 2399, Ap
Sequence 96, Appl
Sequence 88, Appl
Sequence 17, Appl
Sequence 37, Appl
Sequence 17, Appl
Sequence 37, Appl
Sequence 17, Appl
Sequence 37, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 143, App
Sequence 143, App
Sequence 210, App
Sequence 86, Appl
Sequence 86, Appl
Sequence 98, Appl
Sequence 97, Appl
Sequence 1, Appli
Sequence 106, App
Sequence 3, Appli
Sequence 13, Appl
Sequence 100, App
Sequence 15, Appl
Sequence 14, Appl
Sequence 142, App
Sequence 288, App
Sequence 325, App
Sequence 17120, A

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633 44.7 662 6
421 32.0 674 7
1864 24.2 359 8
451 21.2 314 9
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813 17.7 277.5 11
993 17.8 263.5 12
456 10.8 160 13
7805 8.8 130.5 14
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3320 8.7 128.5 16
352 8.7 128.5 17
3391 8.6 128 18
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3186 8.5 127.5 34
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7699 8.5 127.5 41
5739 8.4 125 42
6417 8.4 125 43
6475 8.4 125 44
1086 8.3 123 45

ALIGNMENTS

RESULT 1

US-10-115-899-6

; Sequence 6, Application US/10115899

; Patent No. US20020151025A1

; GENERAL INFORMATION:

; APPLICANT: Ostuka Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Human TSC403 gene and human INGL1 gene

; FILE REFERENCE: Q60193

; CURRENT APPLICATION NUMBER: US/10/115.899

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 09/601,478

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP H10-134679

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: JP H10-73234

; PRIOR FILING DATE: 1998-03-05

; PRIOR APPLICATION NUMBER: JP H10-38133

; PRIOR FILING DATE: 1998-02-03

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 840

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

Alignment Scores:

Pred. No.: 8	Length:
Fragment Score: 21	Matches: 0
Score: 1481.00	Conservative: 0
Percent Similarity: 100.00%	Mismatches: 0
Best Local Similarity: 100.00%	Indels: 0
Query Match: 100.00%	Caps: 0
DB: 12	

US-09-513-365A-1 (1-280) x US-10-115-899-6 (1-840)

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Db	1	ATGTAGGCGCAGCAGCAGCAACTGCTACTCGTCGGCGCGCTCTCTACCGGGAGCGG	60
QY	21	SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis	40
Db	61	AGCCGGCTGCTACCTGCTAGTCGAGACTACCTTGAGTCGTGGAGTCGTGCCCCAC	120
QY	41	AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu	60
Db	121	GACATGCAGAGGAAGTGTCTGCTGCGAGAGCTGCACAAACAATATCAAGAAAGCTTA	180
QY	61	LysGluIleAspAspValTyrGluLysTyrLysGluIleAspAspLeuAsnGlnLysLys	80
Db	181	AAGGAATTTGATGTGCTACGAAATAATATAAGAAAGAAGATGATTTAAACCAAGAA	240
QY	81	ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys	100
Db	241	CGTCACAGCAGCTTCTCCAGAGACACTAATTATAGTCAGAATTTGGAGATGAAAA	300
QY	101	IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu	120
Db	301	ATACAGATTGTTACACAAATGCTCAATTTGGTGGAAAAATCGGCCAAGACAAATGGAGTTA	360
QY	121	HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet	140
Db	361	CACTCACAGTGTTCACAGATCCCTGCTGAAGTGAACGAGCCCTCAGATAAGCAAAAGTG	420
QY	141	AspSerSerGlnProGluArgSerSerArgArgProArgGlnArgThrSerGluSer	160
Db	421	GATTCACGCCAACCAAGAAAGATCTTCAAGAAGACCCCGCAGGCGGACCGAGTGAAGC	480
QY	161	ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu	180
Db	481	CGTGATTTATGTACATGGCAAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAA	540
QY	181	LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla	200
Db	541	AGAAATCCAGTCAGCAAGAAAGAAAGAACCTCCAAAGCCCAAGCAGGAAGGAAGCT	600
QY	201	SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal	220
Db	601	TCACCTGTGTAGTTTGCAATAGATCCTTAATGAACCTACACTACTGCTTATGCAACCAAGTG	660
QY	221	SerTyrGlyGluMetIleGlyCysAspAsnGlnCysProIleGluTrpPheHisPhe	240
Db	661	TCTTTATGGGAGATGATAGGATGTGACAATGAACAGGTGTCCAATTGAAATGGTTTCACTTT	720
QY	241	SerCysValSerLeuThrTyrLysProLysGlyLysTyrTyrCysProLysCysArgGly	260
Db	721	TCATGTGTTTCACTTACCTATAAACCAAGGGGAAATGGTATTGCCCCAAAGTCAGGGGA	780
QY	261	AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg	280
Db	781	GATAATGAGAAACAATGGCAAAAGTCTGAAAGACAAAAGGATAGAGATCGAGG	840

RESULT 2

US-10-115-899-7
; Sequence 7, Application US/10115899
; Patent No. US20020151025A1
; GENERAL INFORMATION:
; APPLICANT: Ostuka Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene

Qy 201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220
 Db 692 TCACCTGTGAGTTGCAATAGATCTTAATGAACCTACATACCTGTTATGCAACCAAGTG 751
 Qy 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240
 Db 752 TCTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCCAATTTGAATGTTTCACTTT 811
 Qy 241 SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly 260
 Db 812 TCATGTCTTCACTTACCTATACCAAGGGGAATGGTATTCCTCCCAAGTGCAGGGGA 871
 Qy 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
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RESULT 3

US-09-968-653A-4
 ; Sequence 4, Application US/09968653A
 ; Publication No. US20030073084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudkov, Andrey V
 ; Garbavstev, Igor
 ; Riabowol, Karl
 ; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/968,653A
 ; FILING DATE: 01-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/006,783A
 ; FILING DATE: 15-JAN-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. US20030073084A1nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 97,837
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-0002
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 873 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 7..813
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-968-653A-4
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 Pred. No.: 2,15e-89 Length: 873
 Score: 853.50 Matches: 161
 Percent Similarity: 75.74% Conservative: 45
 Best Local Similarity: 59.19% Mismatches: 51
 Query Match: 57.63% Indels: 15
 DB: 9 Gaps: 3

US-09-513-365A-1 (1-280) x US-09-968-653A-4 (1-873)
 Qy 18 GlyGluArgSerArgLeuLeuThrCystTyrValGlnAspTyrLeuGluCysValGluSer 37
 Db 25 GGGAGGAGGAGTCCACCTGGTGAAC---TATGTGGAGGAGTACCTGAGGACTCCATCGAGTCC 81
 Qy 38 LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
 Db 82 CTGCTTTCGACTTGCAGAGAAATGCTCGCTGATCGGGAGATCGACCGCGAATAACCAA 141
 Qy 58 GluThrLeuLysGluIleAspValTyrGluLysTyrLysLysGluAspAsnLeu 77
 Db 142 GAGATCTCTGAGGAGTACAGAGTGTCTACAGCGCTTCAGTCGCGACACAGACGGCGG 201
 Qy 78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeu 97
 Db 202 CAGAGCGGGCGATGCTGCATCTGTGCGACGCGCGCTGATCCGCGACGAGAGCTGGGC 261
 Qy 98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
 Db 262 GACGAGAAGATCCAGATCGTCGACGAGATGTGTGAGCTGTGTGAGAACCGCACGCGGCG 321
 Qy 118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu----- 130
 Db 322 GTGACACGCCACGTGGAGCTGTTCCAGCGCGCAGGAGTGGCGCACACAGTGGGCAAC 381
 Qy 131 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnPro 145
 Db 382 AGCGGCAAGTTGGCGGACAGGCGCCATGGCGATGGCGTACGCGCATCTGACAGGCC 441
 Qy 146 GluArgSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHis 165
 Db 442 -----AACACAAGCGCTCACGGCGGCGCAGCAACACGAGAACCGGTGAGAACCGTCC 495
 Qy 166 MetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysSerLysSer 185
 Db 496 AGCAACACGACGACGACGCGCGCGCTCGGGCGCACACCCCAAGAGAGAGGAGGAGGAG 555
 Qy 186 AlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPhe 205
 Db 556 TCCAGAGAGAAGAGCGCTCCAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 615
 Qy 206 AlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet 225
 Db 616 CCCATCGACCCCAACGAAACCCACGCTACTGTCTGTGCAACAGGTCTCTATGGGAGATG 675
 Qy 226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu 245
 Db 676 ATCGGCTGCGACAACGACGAGTGCCTCCATCGAGTGGTTCACACTTCTCGTGGTGGGCTC 735
 Qy 246 ThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThr 265
 Db 736 AATCATAAACCCAGGCGCAAGTGTGTCTCCCAAGTCCCGGGGGGAGAGAGAGAGAGAG 795
 Qy 266 MetAspLysSerThrGluLysThrLysLysAspArg 277
 Db 796 ATGGACAAAGCGCTGGAGAAATCCAAAAAGAGAGG 831

RESULT 4

US-09-764-877-3454
 ; Sequence 3454, Application US/09764877
 ; Patent No. US20020147140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC005
 ; CURRENT APPLICATION NUMBER: US/09/764,877
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 4031
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 3454

QY 164 CysHisMetAlaAsnGlyIleGluAspCysAspGlnProProLysGluLysLysSer 183
Db 544 CGCTCCAGCAACACACGACGAGCGCGCTCGGCGACACCCCAAGAGAGAGGCC 603
QY 184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
Db 604 AAGACCTCAAGAAGAGAGCGCTCCAGGCGCAAGCGGAGGAGCGTCCCTGCC 663
QY 204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
Db 664 GACCTCCCATCCGACCCCAAGCAACGCTACTGTGTGCAACGAGGTCTCTATGG 723
QY 224 GluMetIleGlyCysAspAsnGlnGlnCysProIleGluTrpPheHisPheSerCysVal 243
Db 724 GAGATGATCGCTGCGACACGAGAGTGCCTCCATCGAGTGTTCACCTTCGTCGGTG 783
QY 244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
Db 784 GGCTCTCAATCAATAACCCCAAGGCAAGTGTGTCTCCCAAGTCCCGGGGGAGACGAG 843
QY 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
Db 844 AAGACCATGACAAAGCCCTGGAGAAATCCAAAAAGAGAGG 885

RESULT 6

US-09-968-653A-6
; Sequence 6, Application US/09968653A
; Publication No. US20030073084A1
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; Riabowol, Igor
; TITLE OF INVENTION: p33/TING1 as a Mediator of p53 Signaling
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,653A
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030073084Alban, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..630
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-968-653A-6

Alignment Scores:
Pred. No.: 2,04e-67 Length: 633
Score: 662.00 Matches: 125
Percent Similarity: 75.49% Conservative: 29
Best Local Similarity: 61.27% Mismatches: 36
Query Match: 44.70% Indels: 14
DB: 9 Gaps: 2
US-09-513-365A-1 (1-280) x US-09-968-653A-6 (1-633)
QY 86 LeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr 105
Db 13 GTCAGCGCGCGTGTATCCGACGCCAGGAGCTGGCGACGAGAAGATCCAGATCGTGAGC 72
QY 106 GlnMetLeuGlnLeuValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPhe 125
Db 73 CAGATGGTGGAGCTGTGGAGAACCGCACCGCGAGGTGGACAGCCAGCTGAGCTTTC 132
QY 126 GlnAspProAlaGlu-----SerGluArg 133
Db 133 GAGCGCGACGAGGAGCTGGCGACAGCTGGGCAACAGCGCGAAGGTGGCGGAGCAGG 192
QY 134 AlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArgArgProArg 153
Db 193 CCCAATGGCGATCGGCTAGCGCAGTCTGACAAGCCC-----AACAGCAAGCGCTCACGG 246
QY 154 ArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCys 173
Db 247 CGGACGCGCAACACGAGAACCGCTGAGACCGCTCCAGCAACACCGACGACGACGCGC 306
QY 174 AspAspGlnProProLysGluLysSerLysSerAlaLysLysLysLysLysLysLys 193
Db 307 GCCTCGGGCACACCCAGGAGAGAGCGCCACAGCTCCCAAGAGAGAGAGAGAGAGAG 366
QY 194 AlaLysGlnGluArgGluAlaSerProValIleGluPheAlaIleAspProAsnGluProThr 213
Db 367 GCCAAGCGCGAGCGAGAGCGCTCCCTCGCGACCTCCCTCCCATCGACCCCAACGACCCACG 426
QY 214 TyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCys 233
Db 427 TACTGTCTGTGCAACACGAGTCTCTATGGGAGATGATCGCTGCGGAGTGCAGACGAGTGC 486
QY 234 ProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrp 253
Db 487 CCCATCGAGTGGTTCACCTTCTCGTGGCTGGGCTCAATCATAAACCCCAAGGCAAGTGG 546
QY 254 TyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThr 273
Db 547 TACTGTCCCAAGTCCCGGGGGAGACGAGAGACCATGGACAAAGCCCTGGAGAAATCC 606
QY 274 LysLysAspArg 277
Db 607 AAAAAAGAGAGG 618
RESULT 7
US-09-918-995-37033
; Sequence 37033, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37033
; LENGTH: 421

Alignment Scores:	
Pred. No.:	1.10e-31
Score:	359.00
Percent Similarity:	24.52%
Best Local Similarity:	22.52%
Query Match:	24.24%
DB:	9
Gaps:	11
Indels:	198
Mismatches:	100
Conservative:	53
Matches:	102
Length:	1864

Alignment Scores:	
Pred. No.:	1.10e-31
Score:	359.00
Percent Similarity:	22.52%
Best Local Similarity:	24.22%
Query Match:	24.24%
DB:	9
Gaps:	11
Indels:	198
Mismatches:	100
Conservative:	53
Matches:	102
Length:	1864

US-09-513-365A-1 (1-280) x US-10-037-270-435 (1-1864)

22	ArgLeuLeuThrCys	TyrValGln	AspTyrIleu	GluCysVal	GluSerLeu	ProHis	Asp	41
155	AGGGCGGGAGT	GTGACTAG	AGACTAT	CTGGAA	TGATGAG	CAGCTT	CTCTAT	GGAT
42	MetGlnArg	AsnValSer	ValLeu	ArgGluLeu	AspAsn	LysTyr	GlnGlu	ThrLeu
215	CTCGGGGACCG	CTTCACG	GAATCGG	CAGATG	GACCTGC	GAGTGC	AGAA	TGCAATG
62	GluIleAsp	AspValTyr	GluLysTyr	LysLysGlu	AspLeu	AsnGln	LysLys	---
272	-----GAT	CAACTAGA	CAAAAG	AGCTCAG	TCAATCTTT	TATGAA	TGCAAA	AAAAAT
81	-----Arg	LeuGlnGln	Leu-----	LeuGln	ArgAla	IleLeu	IleAsn	SerGln
323	AAACTG	AGTGGG	GAAGCA	AAATGC	ATCCAT	CAAAAG	AGCTACT	ATAAAGCTTTC
95	GluLeuGly	AspGluLys	IleGlnIle	ValThrGln	MetLeu	GluValGlu	AsnArg	114
383	GAA	GATGC	AGATG	AGAAG	GTTCAG	TGTGG	CAAA	CCAGATATATGACTTGGTAGATCGACAC
442								

RESULT 8
US-10-037-270-435

Db	443	TTGAGAAAAGCTGGATCAGGAAC	TGGCTAAAGTTTAAAAATGGAGCTGGAAGCTGATAATGCT	507
Ov	134	-----	-----	134

; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: T.J.U. Chenghua

APPLICANT: LIU, Chienling
APPLICANT: ASUNDI Vinod

; APPLICANT: ASUNDI, VINOD

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue. Aidong J.

AFFILIANT: Xue, Aiqiong J.
 APPLICANT: Vang Vongphong

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

APPLICANT: Ma, Yunging

; APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPL.TCANT: Tillinaghast, Jo

APPLICANT: WILLIAMS, J.

; APPLICANT: Drmanac, Radojevic, et al.

;; TITLE OF INVENTION: NO. US.

; TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER:

: CURRENT FILING DATE: 2002-

: PRIOR APPLICATION NUMBER: 0

; PRIOR APPLICATION NUMBER: 3000-04-
: PRIOR FILING DATE: 3000-04-

; PRIOR FILING DATE: 2000-04

PRIOR APPLICATION NUMBER: 09-0867

; PRIOR FILING DATE: 2000-01-

; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pt_FL_genes Versi

: SEO ID NO 435

LENGTH: 1864

; LENGTH: 1004

●

Qy	55	LysTyrGlnGlnThrLeuLysGluIleaspValTyrGluLysTyrLysLysGluasp	74
Db	77	AAATACCAAGAGATCTCTGAAGAGCTAGACAGCTGTACGAGCGCTTACGTCGGCAGACA	136
Qy	75	AspLeuasnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln	94
Db	137	GACGGGCGCAGAAGCGCGGATGCTGCACCTGTGTGCAGCGCGCTGATCGCAC -CAG	195
Qy	95	GluLeuGlyaspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluasnArg	114
Db	196	GAGCTGGCGACGAGAAGATCCATGCTGAGCCAGATGGTGGAGCTGGTGAGAACCGC	255
Qy	115	AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg	133
Db	256	ACGCGCAGGTTGGACGCCACGCTGGAGCTGTTTCGAGGCGCAGCAGGAGCTGGCGCACACA	315
Qy	134	AlaSeraspLysAlaLysMetaspSerSerGlnPro-----	145
Db	316	CGGGCCACACGCGCAAGCTGGCGCGGACAGGCCAAAGCGAGCGCGCAGCGCT	375
Qy	146	--GluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgasp	162
Db	376	GACAAAGCCCAACAGCAGCGCTACAGCGCGCAGCGCAACACGAGAAACCGGTGAG	429

RESULT 10
US-09-738-973-146
; Sequence 146, Application US/09738973
; Patent No. US20020110563A1

```

? APPLICANT: Secrist, Heather
? APPLICANT: Indrias, Carol Yoseph
? APPLICANT: Benson, Darin R.
? APPLICANT: Elliot, Mark
? APPLICANT: Mannion, Jane
? APPLICANT: Kalos, Michael D.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
? THERAPY AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.475C9
? CURRENT APPLICATION NUMBER: US/09/738.973
? CURRENT FILING DATE: 2000-12-14
? NUMBER OF SEQ ID NOS: 587
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 146
? LENGTH: 451
? TYPE: DNA
? ORGANISM: Homo sapien
? US-09-738-973-146

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US-09-513-365A-1 (1-280) x US-09-738-973-146 (1-451)
DB:
Query Match: 21.20%
Best Local Similarity: 49.28%
DB: 10
Indels: 11
Gaps: 2
Mismatch: 31

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[illegible]

; CURRENT APPLICATION NUMBER: US/10/04

; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 370
; LENGTH: 7805
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 235885.5
US-10-044-090-370

Alignment Scores:
Pred. No.: 0.000267 Length: 7805
Score: 130.50 Matches: 46
Percent Similarity: 38.60% Conservative: 20
Best Local Similarity: 26.90% Mismatches: 66
Query Match: 8.81% Indels: 39
DB: 12 Gaps: 8

US-09-513-365A-1 (1-280) x US-10-044-090-370 (1-7805)

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QY 122 SerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp 141
DB 1416 TCGTATGTTTTCAGAGCGACGAAGTCTGAACACAGAGGCTGAGGAATCAGACCTGGAC 1475
QY 142 SerSerGlnProGluArgSerArgArgProArgGlnArgThrSerGluSerArg 161
DB 1476 AGTGGCAGTGTCCACAGTCCCTCAGCGCCGCT----- 1508
QY 162 AspLeuCysHisMetAlaAsnGlyLeuGluAspCysAspAspGlnProLysGluLys 181
DB 1509 -----GATGGCCCTGTCCGCCACCAAG 1529
QY 182 LysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSer 201
DB 1530 AAACCTAAAGAGAGCGCGCCAGGAAGGAAGAGAGAGGCTCTGGCGCTGTCTGCAGTG 1589
QY 202 ProValGluPheAlaIleAspProAsnGlu-----ProThrTyrCys---LeuCys 217
DB 1590 GCGGGGAGGAGGAGGTGATGGCTACGAGAGCGGATCACCAGATTACTGTGAGGTGTC 1649
QY 218 AsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluCysProIleGluTrp 237
DB 1650 CAGCAG-----GGTGGGAATATTCTGTGTGACACC-----TGCCCT---CGTGCC 1694
QY 238 PheHisPheSerCysVal-----SerLeuThrTyrLysProLysGlyLysTrpTyrCys 255
DB 1695 TACCACCTCTGTCTGCTTGCCTGATCCTGAGCTTGACCGGGCTCCAGAGGGCAAAATGGAGCTGC 1754
QY 256 ProLysCysArgGlyAsp-----AsnGluLysThrMetAspLysSer 269
DB 1755 CCTCACTGTGAGAGGAGGGGTCCAGTGGGAGGCCAAGAGGAAGAAGAAATCGAAG 1814
QY 270 ThrGluLysThrLysLysAspArgArgSerArg 280
DB 1815 AGGAGGAGGAGGAAGGAAGGGAGAGGAGGAGG 1847
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RESULT 15

US-09-764-864-471
; Sequence 471, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 471
; LENGTH: 915

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (894)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (903)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (905)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (914)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-471

Alignment Scores:
Pred. No.: 1.6e-05 Length: 915
Score: 129.50 Matches: 34
Percent Similarity: 40.77% Conservative: 19
Best Local Similarity: 26.15% Mismatches: 34
Query Match: 8.74% Indels: 43
DB: 10 Gaps: 7

US-09-513-365A-1 (1-280) x US-09-764-864-471 (1-915)

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QY 166 MetAlaAsnGlyLeuGluAspCys-----Asp 174
DB 190 CTGGCGGGGCTGTGAGGAGTGCCTGGCGGAGCGGAGATATGAGGGAGATGTTTCAGAC 249
QY 175 AspGlnProPro-----LysGluLysLysSerLysSerAlaLysLysLysArg 191
DB 250 CCAGAGCTCCAGATGCCGGGAGGACACCAAGTCCGAGAATGGGAG----- 297
QY 192 SerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGlu 211
DB 298 -----AATGCG 303
QY 212 ProThrTyrCysLeuCysAsnGlnValSerTyrGly---GluMetIleGlyCysAspAsn 230
DB 304 CCCATCTACTGCATCTGCCGCAACCGGACATCAACTGCTTCATGATCGGGTGTGACAAC 363
QY 231 GluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLys 250
DB 364 -----TGCAAT---GAGTGGTTCATGGGGACTGCATCCGGATCCTCAGAAGATGGCC 414
QY 251 -----GlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
DB 415 AAGGCCATCCGGGAGTGTGCTGGGAGTGCAGAGAGAGAAAGACCCCAAGCTAGAGATT 474
QY 268 LysSerThrGluLysThrLysLysAspArg 277
DB 475 CGCTATCGGCACAAAGAATGCACGGGAGCGG 504
```

Search completed: June 20, 2003, 04:42:50
Job time : 173 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1046	96.9	1078	4	US-09-601-478-7	Sequence 7, Appli
2	838.4	77.6	840	4	US-09-601-478-6	Sequence 6, Appli
3	825.2	76.4	1154	4	US-09-484-970B-81	Sequence 81, Appl
4	237.4	22.0	873	4	US-09-006-783A-4	Sequence 4, Appli
5	183.8	17.0	1902	2	US-09-258-237-1	Sequence 1, Appli
6	183.8	17.0	1902	2	US-09-258-371-1	Sequence 1, Appli
7	183.8	17.0	1902	3	US-08-569-721A-1	Sequence 1, Appli
8	183.8	17.0	1902	3	US-08-751-230-1	Sequence 1, Appli
9	183.8	17.0	1902	3	US-09-499-082-1	Sequence 1, Appli
10	183.8	17.0	1902	4	US-09-258-372-1	Sequence 1, Appli
11	183.8	17.0	2061	2	US-09-258-371-9	Sequence 9, Appli
12	183.8	17.0	2061	3	US-08-751-230-9	Sequence 9, Appli
13	183.8	17.0	2061	3	US-09-499-082-9	Sequence 9, Appli
14	183.8	17.0	2061	4	US-09-258-372-9	Sequence 9, Appli
15	182.2	16.9	2061	4	US-09-006-783A-2	Sequence 2, Appli
16	182.2	16.9	2061	4	US-09-159-871-1	Sequence 1, Appli
17	174.4	16.1	633	4	US-09-006-783A-6	Sequence 6, Appli
18	95.6	8.9	678	3	US-09-193-286-3	Sequence 3, Appli
19	95.6	8.9	699	3	US-09-195-286-2	Sequence 2, Appli
20	83.6	7.7	451	4	US-09-370-838-146	Sequence 146, App
21	72.4	6.7	7218	1	US-08-232-463-14	Sequence 14, Appl
22	50.6	4.7	860	1	US-07-847-010-18	Sequence 18, Appl
23	49	4.5	593	4	US-09-385-982-252	Sequence 262, App
24	46.8	4.3	6124	4	US-08-213-439B-3	Sequence 3, Appli
25	46.2	4.3	1189	1	US-07-781-034-4	Sequence 4, Appli
26	46.2	4.3	1189	5	PCT-US92-08328-4	Sequence 4, Appli
27	45.8	4.2	19124	2	US-08-487-836B-13	Sequence 13, Appl


```

; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 81
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
; LOCATION: 17-37
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-81

Query Match 76.4%; Score 825.2; DB 4; Length 1154;
Best Local Similarity 97.9%; Pred. No. 1e-206;
Matches 836; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 211 GCTCGGAGCTGACACAAATATCAAGAAACGTTAAAGGAATTTGATGATGCTACGA 270
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 301 GCTCGGACCGTGGGGATCTGCTCGCAACGTTAAAGGAATTTGATGATGCTACGA 360
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 271 AAAATATAAGAAAGAGATGATTTAAACCAAGAAAGCGTCTACAGCAGCTTCTCCAGAG 330
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 361 AAAATATAAGAAAGAGATGATTTAAACCAAGAAAGCGTCTACAGCAGCTTCTCCAGAG 420
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 331 AGCACTAATTAATAGTCAAGATTTGGGAGATGAAAAATACAGATTTGACACAAATGCT 390
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 421 AGCACTAATTAATAGTCAAGATTTGGGAGATGAAAAATACAGATTTGACACAAATGCT 480
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 391 CGAATTGGTGAAATCGGCAAGCAAAATGAGTGTACACACAGTGTTCCTCAAGATCC 450
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 481 CGAATTGGTGAAATCGGCAAGCAAAATGAGTGTACACACAGTGTTCCTCAAGATCC 540
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 451 TGCTGAAAGTGAACGAGCTCAGATAAAGCAAAAGATGGATTCACGCCAACAGAAAGATC 510
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 541 TGCTGAAAGTGAACGAGCTCAGATAAAGCAAAAGATGGATTCACGCCAACAGAAAGATC 600
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 511 TTCAGAGAGACCCCGCAGCAGCAGCAGCAGTGAAGCCGTGATTATGTCACATGGCAAA 570
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 601 TTCAGAGAGACCCCGCAGCAGCAGCAGTGAAGCCGTGATTATGTCACATGGCAAA 660
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 571 TGGGATTGAACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 630
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 661 TGGGATTGAACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 631 AAAGAAAGCTTCCAAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 721 AAAGAAAGCTTCCAAAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 691 TCCTAATGAACACTTACATCTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATGATG 750
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 781 TCCTAATGAACACTTACATCTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATGATG 840
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 751 TGACAATGAACAGTGTCCAAATGAATGTTTCACTTTTCACTTTTCACTTTTCACTTTTCACT 810
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 841 TGACANTGAACAGTGTCCAAATGAATGTTTCACTTTTCACTTTTCACTTTTCACTTTTCACT 900
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 811 ACCAAAGGGGAAATGGTATTCGCCAAAGTGCAGGGGAGATAATGAGAAAAAATGGACAA 870
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 901 ACCAAAGGGGAAATGGTATTCGCCAAAGTGCAGGGGAGATAATGAGAAAAAATGGACAA 960
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 871 AAGTACTGAAAGACAAAAAGGATAGAGATCGAGGTAGTAAGAGGCCATCCACATTTTA 930
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 961 AAGTACTGAAAGACAAAAAGGATAGAGATCGAGGTAGTAAGAGGCCATCCACATTTTA 1020
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111

; US-09-006-783A-4
; Sequence 4, Application US/09006783A
; Patent No. 6297366
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; APPLICANT: Garkavstev, Igor
; APPLICANT: Riadowol, Karl
; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6297366nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..813
US-09-006-783A-4

Query Match 22.0%; Score 237.4; DB 4; Length 873;
Best Local Similarity 59.0%; Pred. No. 8.1e-53;
Matches 462; Conservative 0; Mismatches 291; Indels 30; Gaps 2;

QY 145 CTACGTGCGAGCTACCTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 204
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 48 CTATGTGAGGAGCTACCTTGTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 107
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 205 GTCTGTGCTGCGAGCTGGGACCAAAATATCAAGAAACGTTAAAGGAATTTGATGATGT 264
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 108 CTCGCTGATGCGGAGATCGAGCGGAAATATCAAGAGATCTCTGAAGGAGCTAGACGATG 167
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 265 CTACGAAATATATAGAAAGAGATGATTTAAACCAAGAAACGCTCTACAGCAGCTTCT 324
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111

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Db 695 ACAAAGCCCTGGAGAAATCCAAAAAGAGAG 725

RESULT 6

US-09-258-371-1

Sequence 1, Application US/09258371

Patent No. 5986078

GENERAL INFORMATION:

APPLICANT: Garkavtsev, Igor

APPLICANT: Riabowol, Karl

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR

TITLE OF INVENTION: SUPPRESSOR GENE INGI

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/258,371

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/751,230

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mool, Leslie A.

REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-144

TELEPHONE: 415-854-7400

TELEFAX: 415-854-8275

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1902 base pairs

TYPE: nucleic acid

STRANDEDNESS: Double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 109..741

US-09-258-371-1

Query Match 17.08; Score 183.8; DB 2; Length 1902;

Best Local Similarity 57.08; Pred. No. 1.4e-38;

Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

Qy 237 AAGAAAGCTTAAAGGAATGATGCTCTACGAAAAATATAAGAAAGAGATGATTAA 296

Db 35 AACAGATCCTGAAGGACGTAGACGAGTGCTACGAGCGCTTCAGTCGGCAGACACGCGG 94

Qy 297 ACCAGAGAAGACCTCTACAGAGCTTCCAGAGAGCAGCAATTAATAGTCAAGAAATGG 356

Db 95 CGCAGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 154

Qy 357 GAGATGAAAAATACAGATGTTACACAAATGCTGAAATGGTGGAAAAATCGGCAAGAC 416

Db 155 GCGACGAGAAGATCCAGATGCTGAGCAGATGCTGGAGCTGGTGGAGAACCGCAGCGGC 214

Qy 417 AAATGGAGTTACACTACAGCTGTTCCAAAGATC----- 449

Db 215 AGTGGACACCGCTGGAGCTGTTCCAGGCGGAGGAGCTGGGCGACACAGTGGGCA 274

Qy 450 -CTGCTGAAAGTGAACGAGCTCAGATATAAGCAAGATGGATTCAGCCCAACCAAGA 508

Db 275 ACAGCGGCAAGGTTGGCGGACAGGCCCCAATGCGGATGGGTAGCGAGCTCTGACAAGC 334

Qy 509 TCTTCAAGAA--GACCCCGCAGCGCAGCGGACCGTGAAGCCGTTATTTGTTCACATGG 566

Db 335 CCAACAGCAAGCGCTACGCGGCGCAGCAGACACAGAGACCGTGAGAACCGTCCAGCA 394

Qy 567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAAGAAAAAGAAATCCAAAGTCAGCA 626

Db 395 ACCAGGACACGAGCGCGCTCGGGCGCACACCAAGGAGAGAGGCGCAAGACCTCCA 454

Qy 627 AGAAAAAGAACGCTCCAAAGCCCAAGCAGGAGGAGGAGCTTACCTGTTGAGTTTGCAG 686

Db 455 AGAAGAAGAAGCGCTCCAAAGGCGGCGGAGGAGGAGGCTCCCTGCGGACCTCCCA 514

Qy 687 TAGATCCTAATGAACCTACATACCTTATGCAACCAAGTCTTATGCGGAGAGATGATAG 746

Db 515 TCGACCCCAAGAACCCACCTGCTGTGTGCAACCAAGTCTTATGCGGAGAGATGATCG 574

Qy 747 GATGTGACAATGAACAGTGTCCCAATGAATGGTTTTCATGTTTTCATGTTTTCATCTTACCT 806

Db 575 GCTGCGACAAGGAGTGTCCCAATGAGTGTGTTTCCACTTCTCGTGGGCGCTCAATC 634

Qy 807 ATAAACCAAGGGGAAATGTTATGCCCCCAAGTGCAGGGGAGATATAAGAAAAACATGG 866

Db 635 ATAAACCAAGGGCAAGTGTGTTCTCCCAAGTGCAGGGGAGAGAGGAGGAGGAGGAGG 694

Qy 867 ACAAAGTACTGAAAGACACAAAAAGGATAG 897

Db 695 ACAAAGCCCTGGAGAAATCCAAAAAGAGAG 725

RESULT 7

US-08-569-721a-1

Sequence 1, Application US/08569721a

Patent No. 6037121

GENERAL INFORMATION:

APPLICANT: GARKAVTSEV, Igor

APPLICANT: RIABOWOL, Karl

TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR

TITLE OF INVENTION: SUPPRESSOR GENE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,721a

FILING DATE: 08-DEC-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Mool, Leslie A.

REGISTRATION NUMBER: 37,047

REFERENCE/DOCKET NUMBER: 028722-128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 854-7400

TELEFAX: (650) 854-8275

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1902 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 109..738
US-08-569-721A-1

Query Match 17.0%; Score 183.8; DB 3; Length 1902;

Best Local Similarity 57.0%; Pred. No. 1.4e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

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QY 237 AAGAAAGTTAAAGAAATGATGCTACGAAATATATAGAAAGAGATGATTAA 296
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 35 AACAGATCTGAAGAGCTAGAGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGG 94

QY 297 ACCAGAAAGAACTCTACAGAGCTTCTCCAGAGACACTAATTAATAGTCAAGAA 356
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 CGCAGAAAGGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 154

QY 357 GAGATGAAATATACAGATGTTTACACAAATGCTGAATTTGTTGGAATCGGCA 416
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 GCGACAGAGATCCAGATGCTGAGCCAGATGCTGAGAGAGTGGTGGAGAACCG 214

QY 417 AATGAGTTTACACTCAGAGTGTTCCTCAAGATC----- 449
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 AGGTGACAGCCAGCGCTGCTGAGCGCGAGCGAGCTGGGCGGACAGTGGGCA 274

QY 450 -CTGCTGAAGTGAACGAGCGCTCAGATAAAGCAAGATGGATTCAGCCCAAC 508
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 ACAGCGGCAAGGTTGGCGGCGAGCGGCCCAATGGCGATCGGTAGCGAGTCTG 334

QY 509 TCTTCAAGAA--GACCCCGCAGCGAGCGAGCGAGTGAAGCGGTGATTTATG 566
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 CCAACAGCAAGCGCTCAGCGCGCGAGCGCAACAGAGAACCGGTGAGAACGGT 394

QY 567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTTAAGAAAGAAATCAAG 626
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 ACCAGGACACAGCGCGCGCTCGGGCACACCCCAAGGAGAGAGGCGAGACCT 454

QY 627 AGAAAAAGAAAGCGTCCAGAGCGCAAGAGGAAAGGAGCTTCACCTGTGAGT 686
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 AGAAGAGAGAGCGTCCAGAGCGCAAGGCGGAGCGAGCGGTCCCTCGCCAG 514

QY 687 TAGATCTTAATGAACCTACATCTGTTATGCAACCAAGTGTCTTATGGGAG 746
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 TCGACCCCAACCAAGCGAGTGTCTGTCGCAACCAAGTGTCTTATGGGAGAT 574

QY 747 GATGTGACAAATGAACAGTGTCCCAATGATGATGATGATGATGATGATGAT 806
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 8

US-08-751-230-1

Sequence 1, Application US/08751230

Patent No. 6117633

GENERAL INFORMATION:

APPLICANT: Garkavtsev, Igor

APPLICANT: Riabowol, Karl

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR

TITLE OF INVENTION: SUPPRESSOR GENE IN1

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 109..741
US-08-751-230-1

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Query Match 17.0%; Score 183.8; DB 3; Length 1902;
Best Local Similarity 57.0%; Pred. No. 1.4e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

QY 237 AAGAAAGTTAAAGAAATGATGCTACGAAATATATAGAAAGAGATGATTAA 296
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 35 AACAGATCTGAAGAGCTAGAGAGTCTACGAGCGCTTCAGTCGCGAGACAGCGGG 94

QY 297 ACCAGAAAGAACTCTACAGAGCTTCTCCAGAGACACTAATTAATAGTCAAGAA 356
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 CGCAGAAAGGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 154

QY 357 GAGATGAAATATACAGATGTTTACACAAATGCTCGAATTTGTTGGAATCGGCA 416
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 GCGACAGAGATCCAGATGCTGAGCCAGATGCTGAGAGAGTGGTGGAGAACCG 214

QY 417 AATGAGTTTACACTCAGAGTGTTCCTCAAGATC----- 449
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 AGGTGACAGCCAGCGCTGCTGAGCGCGAGCGAGCTGGGCGGACAGTGGGCA 274

QY 450 -CTGCTGAAGTGAACGAGCGCTCAGATAAAGCAAGATGGATTCAGCCCAAC 508
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 ACAGCGGCAAGGTTGGCGGCGAGCGGCCCAATGGCGATCGGTAGCGAGTCTG 334

QY 509 TCTTCAAGAA--GACCCCGCAGCGAGCGAGCGAGTGAAGCGGTGATTTATG 566
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 CCAACAGCAAGCGCTCAGCGCGCGAGCGCAACAGAGAACCGGTGAGAACGGT 394

QY 567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTTAAGAAAGAAATCAAG 626
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 ACCAGGACACAGCGCGCGCTCGGGCACACCCCAAGGAGAGAGGCGAGACCT 454

QY 627 AGAAAAAGAAAGCGTCCAGAGCGCAAGAGGAAAGGAGCTTCACCTGTGAGT 686
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 AGAAGAGAGAGCGTCCAGAGCGCAAGGCGGAGCGAGCGGTCCCTCGCCAG 514

QY 687 TAGATCTTAATGAACCTACATCTGTTATGCAACCAAGTGTCTTATGGGAG 746
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 TCGACCCCAACCAAGCGAGTGTCTGTCGCAACCAAGTGTCTTATGGGAGAT 574

QY 747 GATGTGACAAATGAACAGTGTCCCAATGATGATGATGATGATGATGATGAT 806
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Query Match	17.0%;	Score 183.8;	DB.3;	Length 1902;
Best Local Similarity	57.0%;	Pred. No. 1.4e-38;		
Matches 394;	Conservative 0;	Mismatches 267;	Indels 30;	Gaps 2;
QY 237	AAGAAACGTTTAAAGGAAATTTGATGATCTACGAAAAATAATAGAAAGACGATGATTAA	296		
Db 35	AACAGATCCCGAAGGAGCTAGACGAGTGCATACGACGCGTTTCAGTTCGGAGACACACGGGG	94		

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RESULT 10
US-09-258-372-1
; Sequence 1, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGL
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,230

```

```

: FILLING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: MOOL, Leslie A.
: REGISTRATION NUMBER: 37,047
: REFERENCE/DOCKET NUMBER: 028722-144
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-854-7400
: TELEFAX: 415-854-8275
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1902 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 109..741
: US-09-258-372-1

Query Match 17.08; Score 183.8; DB 4; Length 1902;
Best Local Similarity 57.08; Pred. No. 1.4e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

QY 237 AAGAAAGCTTTAAAGGAAATTTGATGATCTCTACGAAAAATATAAGAAAGAAAGATGATTAA 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 35 AACAGATCTTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGACAGACGCGGG 94

QY 297 ACAGAGAAGAAAGCTCTACAGCAGCTTCTCAGAGAGCAGCACTAAATTAGTCAAGAATTGG 356
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 95 CGGAGAGCGCGCGGATGCTCAGCTGTGTGAGCGCGCTGATCCGAGCGCAGGAGCTGG 154

QY 357 GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAATTCGGGCAAGAC 416
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 155 GCACGAGAGAATCCAGATCGTGAGCCGATGGTGGAGCTGGTGGAGAACCGCACGCGGC 214

QY 417 AAATGGAGTTTACACTCAAGTGTTTCCAAAGATC----- 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 AGGTGGACAGCCACGTGGAGCTGTTGAGCGCAGCAGGAGCTGGGCGCACACAGTGGGCA 274

QY 450 -CTGCTCAAGTGAACGAGCCTCAGATAAGCAAGATGGATTCAGCCCAACCAAGAAGA 508
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 ACAGCGCAAGTTGGCGGAGCAGGCCCAATGGCGATGGGTAGCGAGTGTGACAAGC 334

QY 509 TCTTCAAGAA--GACCCTCGAGCAGCGGACCTGAAAGCCGTGATTTATGTCAATGG 566
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 CCAACAGCAAGCGCTCACGCGCGCAGCGCAACACAGAACCGGTGAGAACCGCTCCAGCA 394

QY 567 CAATGGGATTGAAGACTGTGATGATCAGCCACTTAAAGAAAGAAATTCGAAGTCAGCAA 626
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 395 ACCACGACCACGACGAGCGGCGCTCGGGCACACCCCAAGAGAGAAGCGCCAAAGACCTCCA 454

QY 627 AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGAGGCTTCACTCTGTTGAGTTTGCAG 686
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 AGAAGAAGAGCGCTCCAAGGCCAAGCGGAGCGAGAGGCGTCCCTTCGCGACCTCCCCA 514

QY 687 TAGATCCTTAATGAACCTTACACTGCTTTATGCAACCAAGTGTCTTATGGGAGATGATAG 746
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 515 TCGACCCCAACGAAACCCAGCTACTGTCTGTGCAACAGGCTCTCTATGGGAGATGATCG 574

QY 747 GATGTGACATGAACAGTGTCCAAATTGAATGGTTTTCATTTTCATGTGTTTCACTTACCT 806
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 575 GCTGCGACACAGCAGAGTGGCCCATCGAGTGGTTCACCTTCTCTGCTGGGCTCAATC 634

QY 807 ATAAACCAAGGGAATGTTATGGCCAAAGTGCAGGGGAGATATATGAGAAACAAATGG 866
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 635 ATAAACCAAGGCAAGTGTACTGTCTCCCAAGTGCCTGGGGGAGACGAGAACCAATGG 694

QY 867 ACAAAAGTACTGAAAGACAAAAAAGGATAG 897
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Db 695 ACAAAAGCCCTGGAGAAATCCAAAAAAGAGAG 725

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RESULT 11
 US-09-258-371-9
 : Sequence 9, Application US/09258371
 : Patent No. 5986078
 : GENERAL INFORMATION:
 : APPLICANT: Garkavtsev, Igor
 : APPLICANT: Riabowol, Karl
 : TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
 : TITLE OF INVENTION: SUPPRESSOR GENE INGI
 : NUMBER OF SEQUENCES: 23
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Burns, Doane, Swecker & Mathis
 : STREET: 699 Prince Street
 : CITY: Alexandria
 : STATE: VA
 : COUNTRY: USA
 : ZIP: 22313-1404
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/258,371
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/751,230
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Moel, Leslie A.
 : REGISTRATION NUMBER: 37,047
 : REFERENCE/DOCKET NUMBER: 028722-144
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-854-7400
 : TELEFAX: 415-854-8275
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2061 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 16..900
 : US-09-258-371-9

	Query Match	17.0%;	Score 183.8;	DB 2;	Length 2061;
	Best Local Similarity	57.0%;	Pred. No. 1.4e-38;		
	Matches 394;	Conservative 0;	Mismatches 267;	Indels 30;	Gaps 2;
QY	237	AAGRAACGTTAAAGCGAATTGATCATGTCTACGAAAATATATAAGAAAGAAAGATGATTAA	296		
Db	194	AACAGATCCTGAAGGAGCTAGACAGGTCTACGAGCGCTTCAGTCGGGAGACACACGGG	253		
QY	297	ACCAAGAAACACGCTCTACGACGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAATTGG	356		
Db	254	CGCAGAGCGCGGATGCTGCACTGTGTGCAGCGCGGCTGATCCGACGCCAGGAGCTGG	313		
QY	357	GAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAAATCGGCAAGAC	416		
Db	314	CGCAGAGAGAATCCAGATCGTGAGCCAGATGGTGGAGCTGTTGGAGAACCCGCACGGCG	373		
QY	417	AAATGGAGTTACACTCAAGTGTTCGAAGATC-----	449		
Db	374	AGGTGGACGCCAGTGGAGCTGTTTCGAGGGCCAGCAGGAGCTGGGCGACACAGTGGGCA	433		
QY	450	-CTGCTGAAGTGAACGAGCCTCAGATAACCAAGATGGATTCCAGCCACCACGARAAGA	508		
Db	434	ACAGCGCAAGTTGGCGGACAGGCCCAATGCGGATGCGGTAGCGAGCTGTCAACAAG	493		
QY	509	TCATTCAAGAA--GACCCCGAGGACGGGACCCAGTGAAGCCGTGATTATGTGCATCATGG	566		

Db 494 CCAACAGCAACCGCTACGGCGGCGCAACCAACGAGAACCGTGAGAACCGCTCCAGCA 553
Qy 567 CAATGGGATGAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCCAAGTCAGCA 626
Db 554 ACCAGCAGCAGCAGCGCGCTCGGCGCACCAAGGAGAGAGGAGGAGGAGGAGGAGGAG 613
Qy 627 AGAAAGAAAGCGCTCCAGGCCCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 686
Db 614 AGAAGAGAGCGCTCCAGGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
Qy 687 TAGATCTTAATGAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATAG 746
Db 674 TCGACCCCAAGCAACCCACGACTGCTGTGTCACACAGGTCCTTATGGGAGATAG 733
Qy 747 GATGTGACAAATGAACAGTGTCCAAATGAATGTTTTCACCTTTTTCACCTTACCT 806
Db 734 GCTGGACACGACGAGTGCCTCCATCGAGTGTTCACCTTCTGTCGGGGGCTCAATC 793
Qy 807 ATAAACCAAGGGGAAATGGTATTCGCCCAAGTGCAGGGGAGATTAATGAGAAACAATGG 866
Db 794 ATAAACCAAGGGGAAATGGTATTCGCCCAAGTGCAGGGGAGATTAATGAGAAACAATGG 853
Qy 867 ACAGAGTACTGAAAGACAAAGAGATAG 897
Db 854 ACAGAGCTCGAGAAATCCAAAGAGAG 884

RESULT 12
US-08-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: US/08/751,230
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569721
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mool, Leslie A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 028722-144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS

; LOCATION: 16..900
US-08-751-230-9
Query Match 17.0%; Score 183.8; DB 3; Length 2061;
Best Local Similarity 57.0%; Pred. No. 1.4e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;
Qy 237 AAGAAACCTTAAAGGAAATTTGATGATGCTACGAAATAATATAAGAAAGAAAGATGATTTAA 296
Db 194 AACAGATCTTGAAGAGCTAGACGAGTCTACGAGCGCTTCAGTCGCGAGACAGACGGGG 253
Qy 297 ACCAGAGAAACGCTTACAGAGCTTTCAGAGAGAGCAGCTTAATTAATAGTCAAGAAATGG 356
Db 254 CGCAGAGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
Qy 357 GAGATGAAATAATACAGATTTTACACAAATGCTTGAATTTGTTGAAATCGGGAACAG 416
Db 314 GCGAGGAGAGATCCAGATCGTGAGCCAGATGGTGAGAGCTGGTGAGAGAACCGCAGCGGC 373
Qy 417 AAATGGAGTTTACACTCACAGTGTTCCTCAAGATC----- 449
Db 374 AGGTGGACAGCCACGTGGAGCTGTTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGCA 433
Qy 450 -CTGCTGAAAGTGAACGAGCCTCAGATTAAGCAAGATGATTCAGGCCACACCAAGAAAGA 508
Db 434 ACAGCGCAAGGTTGGCGCGGACAGGCGCAATGGCGATCGGCTAGCGAGTCTGCACAGC 493
Qy 509 TCTTCAAGAA--GACCCCGCAGGCGAGCGACAGTGAAGCGCGTATTATGTCACATGG 566
Db 494 CCAACAGCAAGCGCTACGCGGCGCAGCCACACAGAGAACCGTGAGAACCGGCTCCAGCA 553
Qy 567 CAAATGGGATTTGAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCCAAGTCAGCAA 626
Db 554 ACCAGCAGCAGCAGCGCGCTCGGCGCACACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAG 613
Qy 627 AGAAAGAAACGCTTCCAGGCGCAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 686
Db 614 AGAAGAGAGCGCTTCCAGGCGCAAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
Qy 687 TAGATCTTAAATGAACCTACATGCTTATGCAACCAAGTGTCTTATGGGAGATAG 746
Db 674 TCGACCCCAAGCAACCCACGACTGCTGTGTCACACCGTCTCTTATGGGAGATAGTCG 733
Qy 747 GATGTGACAAATGAACAGTGTCCAAATGAATGATGTTTTCACCTTTTTCACCTTACCT 806
Db 734 GCTGGCAACAGCAGGAGTGCCTCCATCGAGTGTTCACCTTCTGTCGGGGGCTCAATC 793
Qy 807 ATAAACCAAGGGGAAATGGTATTCGCCCAAGTGCAGGGGAGATTAATGAGAAACAATGG 866
Db 794 ATAAACCAAGGGGAAATGGTATTCGCCCAAGTGCAGGGGAGATTAATGAGAAACAATGG 853
Qy 867 ACAGAGTACTGAAAGACAAAGAGATAG 897
Db 854 ACAGAGCTCGAGAAATCCAAAGAGAG 884

RESULT 13
US-09-499-082-9
; Sequence 9, Application US/09499082
; Patent No. 6143522
; GENERAL INFORMATION:
; APPLICANT: Helbing, Karen C.
; APPLICANT: Riabowol, Karl
; APPLICANT: Johnston, Randall N.
; APPLICANT: Garkavtsev, Igor
; TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

Qy	687	TAGATCCTAATAAGAACTCATACACTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAG	746
Db	674	TCGACCCCAACGAAACCCACGTACTGTCTGTGCAACCAAGTCTCCTATGGGAGATGATCG	733
Qy	747	GATGTGCAAAAGAACACGTGTCCATTGAAATGGTTTCACITTTTCATGTGTTTCACTTACCT	806
Db	734	GCTGGGACAACGACGAGTGCSCCCATCGAGTGGTTTCCACTTCTCGTGGTGGGGCTCAATC	793
Qy	807	ATAAACCAAAAGGGGAAATGGTATTGCCCAAAAGTCGACGGGGAGATATATGAGAAAAACAATGG	866
Db	794	ATAAACCCNAGGCAAGTGGTACTGTGCCAAGTCCCGGGGGGAGACGAGAACCACTGG	853
Qy	867	ACAAAAGTACTGAAAAGACAAAAAGGATAG	897
Db	854	ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG	884

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RESULT 14
US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
; APPLICANT: Garkavtsev, Igor
; APPLICANT: Rabadowl, Karl
; TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENE INGI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version. #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,372

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version.#1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MOOL, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO.: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 16..900
PS-09-258-372-9

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Query Match 17.0%: Score 183.8: DB 4: Length 2061:

Best Local Similarity 57.0%; Pred. No. 1.4e-38;
Matches 394; Conservative 0; Mismatches 267; Indels 30;

QY 237 AAGAACGTTAAACGAAATTGTATCATGTCTACGAAAAATATAAGAAAAGAAGAT
|| | | ||||| | | | | ||||| | | |
Dp 194 AACAGATCCTGAAGSAGCTAGACCAAGTGTCTACGACGGCTTCAGTCGCGAGACA

db 194 AACAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGGAGAGACA

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Qy 297 ACCAGAGAAACGCTCTACAGCAGCTTCTCCAGAGAGACACTAAATTAATAGTCAAGAAATTGG 356
Db 254 CGCAGAAAGCGCGGCTCTGCTAGTGTGCGAGCGCGCTGATCCGCGAGCAGAGCTGG 313
Qy 357 GAGATGAAAAATACAGATGTTTACACAAATGCTCGAATGGTGGGAAATCGGCGACAGC 416
Db 314 GCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGAGAAACCGCAGCGGC 373
Qy 417 AAATGGAGTTACACTACAGCTGTTTCCAAGATC----- 449
Db 374 AGTGGACACCGCTGAGCTGTTTCCAGGCGCAGCAGGAGCTGGCGGACACAGTGGCA 433
Qy 450 -CTGCTGAAAGTGAACGAGCTCAGATAAAGCAAGATGGATTCCAGCAACACAGAAAGA 508
Db 434 ACAGCGCAAGCTGAGCGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Qy 509 TCTTCAGAA--GACCCCGCAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 566
Db 494 CCAACAGCAAGCGCTCAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 553
Qy 567 CAAATGGATGAAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCCAAGTCAGCAA 626
Db 554 ACCAGACCGCAGCAGCGCGCTTCCAGGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
Qy 627 AGAAAGAAACGCTCAAGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 686
Db 614 AGAAGAAAGCGCTCCAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
Qy 687 TAGATCTTAATGAACCTTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGAGATAG 746
Db 674 TCGACCCCAACGAAACCGCTGCTGTGTCGACCAAGTGTGTGAGAGTGTGTGAGAGTGTGTGAG 733
Qy 747 GATGTGCAATGAACAGTGTCCAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 806
Db 734 GCTGCGCAACGAGCAGCTGCGCCATCGAGTGTGTTCCACTTCTGCTGCTGCTGCTGCTGCTGCT 793
Qy 807 ATAAACCAAGGGAATGTTATGCCCCAAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 866
Db 794 ATAAACCAAGGGAATGTTATGCCCCAAAGTGTGTCGACCAAGTGTGTCGACCAAGTGTGTCGAC 853
Qy 867 ACAAAGTACTGAAAGACAAAGGATAG 897
Db 854 ACAAAGCCTGGAGAAATCCAAAAAGAGAG 884

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RESULT 15

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us-09-006-783A-2
; Sequence 2, Application US/09006783A
; Patent No. 6297366
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; APPLICANT: Garbavstev, Igor
; APPLICANT: Riabowol, Karl
; TITLE OF INVENTION: p33/Ingl as a Mediator of p53 Signaling
; TITLE OF INVENTION: Pathway
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,783A
; FILING DATE: 15-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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; NAME: No. 6297366nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 97,837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..897
; US-09-006-783A-2

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Query Match 16.9%; Score 182.2; DB 4; Length 2061;
Best Local Similarity 56.9%; Pred. No. 3.7e-38;
Matches 393; Conservative 0; Mismatches 268; Indels 30; Gaps 2;
Qy 237 AAGAAACGTTAAAGGAAATTCATGATGCTCTACGAAAAATATAAGAAAGAAAGATGATTTAA 296
Db 194 AACAGATCTCTGAAGCGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGCGAGACAGCGGG 253
Qy 297 ACCAAGAAACGCTCTACAGCAGCTTCTCCAGAGAGCAGCACTAATTAATAGTCAAGAAATTGG 356
Db 254 CGCAGAAAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
Qy 357 GAGATGAAATTAACAGATGTTTACAAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCA 416
Db 314 GCGACGAGAAATCCAGATCTGAGCCAGATGCTGAGAGTGTGTGAGAGTGTGTGAGAGTGTGTGAG 373
Qy 417 AAATGGATGATACACTACAGTGTTCCTCAAGATC----- 449
Db 374 AGTGGACAGCAGCTGAGCTGTTCCAGGCGCAGCAGGAGCTGGCGGACACAGTGGGCA 433
Qy 450 -CTGCTGAAAGTGAACGAGCTCAGATAAAGCAAGATGGATTCCAGCAACACAGAAAGA 508
Db 434 ACAGCGCAAGTGTGGCGGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Qy 509 TCTTCAGAA--GACCCCGCAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 566
Db 494 CCAACAGCAAGCGCTCAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 553
Qy 567 CAAATGGATGAAAGACTGTGATGATCAGCCACCTTAAAGAAAGAAATCCCAAGTCAGCAA 626
Db 554 ACCAGACCGCAGCAGCGCGCTTCCAGGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
Qy 627 AGAAAGAAACGCTCCAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 686
Db 614 AGAAGAAAGCGCTCCAAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
Qy 687 TAGATCTTAATGAACCTTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGAGATAG 746
Db 674 TCGACCCCAACGAAACCGCTGCTGTGTCGACCAAGTGTGTGAGAGTGTGTGAGAGTGTGTGAG 733
Qy 747 GATGTGCAATGAACAGTGTCCAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 806
Db 734 GCTGCGCAACGAGCAGTGTGCGCCATCGAGTGTGTTCCACTTCTGCTGCTGCTGCTGCTGCTGCT 793
Qy 807 ATAAACCAAGGGAATGTTATGCCCCAAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 866
Db 794 ATAAACCAAGGGAATGTTATGCCCCAAAGTGTGTCGACCAAGTGTGTCGACCAAGTGTGTCGAC 853
Qy 867 ACAAAGTACTGAAAGACAAAGGATAG 897
Db 854 ACAAAGCCTGGAGAAATCCAAAAAGAGAG 884

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Search completed: June 20, 2003, 02:42:11
Job time : 85 secs

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	1046	96.9	1078	12	US-10-115-899-7	Sequence 7, Appli	
2	838.4	77.6	840	12	US-10-115-899-6	Sequence 6, Appli	
3	378.4	35.0	421	9	US-09-918-995-37033	Sequence 37033, A	
4	237.4	22.0	873	9	US-09-968-653A-4	Sequence 4, Appli	
5	183.4	17.0	8487	10	US-09-764-877-3454	Sequence 3454, Ap	
6	182.2	16.9	2061	9	US-09-968-653A-2	Sequence 2, Appli	
7	174.4	16.1	633	9	US-09-968-653A-6	Sequence 6, Appli	
8	91.6	8.5	1864	9	US-10-037-270-435	Sequence 435, App	
9	83.6	7.7	451	9	US-09-854-133-146	Sequence 146, App	
10	83.6	7.7	451	10	US-09-738-973-146	Sequence 146, App	
11	66.6	6.2	993	10	US-09-801-368-257	Sequence 257, App	
12	62	5.7	813	9	US-09-938-842A-1178	Sequence 1178, Ap	
13	56.8	5.3	456	9	US-09-918-995-16047	Sequence 16047, A	
C 14	51.6	4.8	393	10	US-09-960-352-4582	Sequence 4582, Ap	
C 15	50.8	4.7	361	10	US-09-919-580-114	Sequence 114, App	
C 16	49	4.5	593	9	US-09-871-161-262	Sequence 262, App	
C 17	48.8	4.5	277	10	US-09-960-352-12673	Sequence 12673, A	
18	48	4.5	5520	9	US-10-001-887-43	Sequence 43, Appli	
C 19	48.4	4.4	527	9	US-10-108-698-863	Sequence 863, App	

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QY 121 GGAGCGAGCGGCTCCTCACCTGCTACGTCGAGGACTACCTTGAGTGGTGGAGTCGCT 180
Db 145 GGAGCGAGCGGCTCCTCACCTGCTACGTCGAGGACTACCTTGAGTGGTGGAGTCGCT 204
QY 181 GCGCCACGACATGACAGGAAGCTGCTGCTGCGAGAGCTGGACAAATATCAAGA 240
Db 205 GCGCCACGACATGACAGGAAGCTGCTGCTGCGAGAGCTGGACAAATATCAAGA 264
QY 241 AACGTTAAAGGAAATGATGATGCTACGAAATATTAAGAAAGAGATGATTTAAACA 300
Db 265 AACGTTAAAGGAAATGATGATGCTACGAAATATTAAGAAAGAGATGATTTAAACA 324
QY 301 GAAGAACGCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGGGAGA 360
Db 325 GAAGAACGCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGGGAGA 384
QY 361 TGAAAAATACAGATTGTTACACAAATGCTGAAATGGTGGAAATCGGGCAAGACAAT 420
Db 385 TGAAAAATACAGATTGTTACACAAATGCTGAAATGGTGGAAATCGGGCAAGACAAT 444
QY 421 GGAGTTACACTCACAGTGTTCACAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC 480
Db 445 GGAGTTACACTCACAGTGTTCACAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGC 504
QY 481 AAAGTGGATCCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGCAGCGGACAG 540
Db 505 AAAGTGGATCCAGCAACCAAGAAAGATCTTCAAGAAAGCCCGCAGCAGCGGACAG 564
QY 541 TGAAGCCGCTGATTATGTCACATGCAATGGGATTGAAGCTGATGATCAGCCACC 600
Db 565 TGAAGCCGCTGATTATGTCACATGCAATGGGATTGAAGCTGATGATCAGCCACC 624
QY 601 TAAAGAAAGAAATCCAACTCAGCAAGAAAGAAACGCTCCAGGCCCAAGCAGGAAG 660
Db 625 TAAAGAAAGAAATCCAACTCAGCAAGAAAGAAACGCTCCAGGCCCAAGCAGGAAG 684
QY 661 GGAAGCTTCACTGTTGAGTTGCAATAGATCCTATGAACCTACATAGTCTGTTATGCAA 720
Db 685 GGAAGCTTCACTGTTGAGTTGCAATAGATCCTATGAACCTACATAGTCTGTTATGCAA 744
QY 721 CCAAGTGTCTTATGGGAGATGATAGGATGTGACATGAACAGTGTCCCAATGCAATGGTT 780
Db 745 CCAAGTGTCTTATGGGAGATGATAGGATGTGACATGAACAGTGTCCCAATGCAATGGTT 804
QY 781 TCACCTTTTCATGTTTTCATCTACCTATAAACCAGGGAATGGTATTGCCAAAGTG 840
Db 805 TCACCTTTTCATGTTTTCATCTACCTATAAACCAGGGAATGGTATTGCCAAAGTG 864
QY 841 CAGGGGAGATATGAGAAACCAATGGACAAAAGTACTGAAAGACAAAAGGATAGAAG 900
Db 865 CAGGGGAGATATGAGAAACCAATGGACAAAAGTACTGAAAGACAAAAGGATAGAAG 924
QY 901 ATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTATTGCTTTTATATAATTCGTT 960
Db 925 ATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTATTGCTTTTATATAATTCGTT 984
QY 961 TCGTTTCAGAAATGTTTATAGGTAATGCATAAGACTATGCAATAATTTTAAATCATTA 1020
Db 985 TCGTTTCAGAAATGTTTATAGGTAATGCATAAGACTATGCAATAATTTTAAATCATTA 1044
QY 1021 GTATTAAATGGTATTAAGAAAGTGTGTACTTTG 1054
Db 1045 GTATTAAATGGTATTAAGAAAGTGTGTACTTTG 1078

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RESULT 2
 US-10-115-899-6
 ; Sequence 6, Application US/10115899
 ; Patent No. US20020151025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
 ; FILE REFERENCE: Q60193

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; CURRENT APPLICATION NUMBER: US/10/115,899
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/601,478
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP H10-134679
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: JP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: JP H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human embryonic brain cDNA library
; US-10-115-899-6

Query Match      77.6%; Score 838.4; DB 12; Length 840;
Best Local Similarity 99.9%; Pred. No. 1e-194;
Matches 839; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 68 ATGTTAGGCGCAGCAGCAGCAACTGTACTCTCGGCTCGCTCTGACCGGGGAGCGG 127
Db 1 ATGTTAGGCGCAGCAGCAGCAACTGTACTCTCGGCTCGCTCTGACCGGGGAGCGG 60
QY 128 AGCCGGCTGCTCACCTGCTACGTGCGAGGACTACCTTGAGTGGTGGAGTCGCTGCCCCAC 187
Db 61 AGCCGGCTGCTCACCTGCTACGTGCGAGGACTACCTTGAGTGGTGGAGTCGCTGCCCCAC 120
QY 188 GACATGCGACAGCAAGCTGTCTGTGCTGCGAGAGCTGACCAACAATAATCAAGAAAGCTTA 247
Db 121 GACATGCGAGCAAGCTGTCTGTGCTGCGAGAGCTGACCAACAATAATCAAGAAAGCTTA 180
QY 248 AAGGAAATGTGATGTCTTACGAAAAATATAAGAAAGAGATGATTTAAACCAAGAGAA 307
Db 181 AAGGAAATGTGATGTCTTACGAAAAATATAAGAAAGAGATGATTTAAACCAAGAGAA 240
QY 308 CGCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGGGAGATGAAAA 367
Db 241 CGCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATGGGAGATGAAAA 300
QY 368 ATACAGATGTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGCAAGACAAATGGAATTA 427
Db 301 ATACAGATGTTTACACAAATGCTCGAATTTGGTGGAAAAATCGGCAAGACAAATGGAATTA 360
QY 428 CACTCACAGTGTTCACAGATCCTGCTGAAAGTGAACGAGCCTCAGATTAAGCAAGATG 487
Db 361 CACTCACAGTGTTCACAGATCCTGCTGAAAGTGAACGAGCCTCAGATTAAGCAAGATG 420
QY 488 GATTCAGCCACACAGAAAGATCTTCAAGAACCCCGCAGCGCCGAGGACCAAGTGAAGC 547
Db 421 GATTCAGCCACACAGAAAGATCTTCAAGAACCCCGCAGCGCCGAGGACCAAGTGAAGC 480
QY 548 CGTGATTTATGTCACATGCGCAATGGGATTTGAAGCTGTGATGATCAGCCACCTAAAGAA 607
Db 481 CGTGATTTATGTCACATGCGCAATGGGATTTGAAGCTGTGATGATCAGCCACCTAAAGAA 540
QY 608 AAGAAATCCAGTCAGCAAGAAAGAAACCGCTCAAGGCCAAGCAGGAGGAGGAGCT 667
Db 541 AAGAAATCCAGTCAGCAAGAAAGAAACCGCTCAAGGCCAAGCAGGAGGAGGAGCT 600
QY 668 TCACCTGTTGAGTTTGCATAGATCCTAATGAACCTACATCTGCTTATGCAACCAAGTG 727
Db 601 TCACCTGTTGAGTTTGCATAGATCCTAATGAACCTACATCTGCTTATGCAACCAAGTG 660
QY 728 TCTTATGGGAGATGATAGGATGTGACATGAACAGTGTCCAAATTTGAATTTTCACTTT 787
Db 661 TCTTATGGGAGATGATAGGATGTGACATGAACAGTGTCCAAATTTGAATTTTCACTTT 720
QY 788 TCATGTGTTTCACTTACCTATATAACCAAGGGGAAATGCTATTTGCCCAAGTGCAGGGGA 847

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Db 721 TCATGTGTTTCACTTACTCTATATAACCAAGGGGAAATGGTATTGCCCAAGTGCAGGGA 780

QY 848 GATATGAGAAACAACATGTCGACAAAAGTACTGAAAGACAAAAAGATAGAACATCGCGG 907

Db 781 GATAATGAGAAACAATGGACAAAAGTACTGAAAGACAAAAAGATAGAACATCGCGG 840

RESULT 3

```

US-09-918-995-37033
; Sequence 37033, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQ
; TITLE OF INVENTION: FROM VARIOUS CDNA LIB
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37033
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(421)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37033

```

Query Match	35.08;	Score 378.4;	DB 9;	Length 421;
Best Local Similarity	93.88;	Pred. No. 1.4e-82;		
Matches 394; Conservative	0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	606	AAAAGAAATCCAAGTCAGCAAGAAGAAAAACGCTCCAAAGGCCAACGACGAAAGGAAG	665	
Db	1	AAAAGAAATCCTAGTCAGCAAGANYPAGAAACTCTCCGAGGCCACCACGAAAGGAAG	60	
QY	666	CTTCACTGTGTGAGTTTGCAATAGATCTCTAATGAACCTACATACTGCTTATGCACCAAG	725	
Db	61	CTTCACTGTGTGAGTTTGCAATAGATCTCTAATGAACCTACATACTGCTTATGCACCAAG	120	
QY	726	TGCTTATGGGAGATCATAGGATGTGCACAATGNACAGTGTCCCAATTGAATGGTTTCACT	785	
Db	121	TGCTTATGGGAGATCATAGGATGTGCACAATGNACACCGTCCCAATTGAGTGGATTCAC	180	
QY	786	TTTTATGTGTTTTCACCTTACCTATAAACCAGGGGAAATGGTATPGCCCAAAGTGCAGGG	845	
Db	181	TTTTATGTGTTTTCACCTTACCTATAAACCAGGGGAAATGGTATPGCCCACAGTGCAGG	240	
QY	846	GAGATATGAGAAAAACAATGGCAAAAAGTACTGNAAGACAAAAAAGGATAGAAGATCGA	905	
Db	241	GAGATATGAGAAAAACAATGGCAAAAAGTACTGATAAGACAAAAAAGCGATAGAAGATCGA	300	
QY	906	GGTAGTAAGGCCATCCACATTTTAAAGGGTATTGTCCTTTATATAATTCTGTTGCTT	965	
Db	301	GGTAGTAAGGCCATCCACATTTTAAAGGGTATTGTCCTTTATATAATTCTGTTGCTT	360	
QY	966	TCAGAAATGTTTTAGGGTAAATGCATAAGACATATGCAATAATTTTTTAATCATTTAGTATT	1025	
Db	361	TCAGAAATGTTTTAGGGTAAATGCATAATATGCTTAAATTTCTTAATCATTTAGTATT	420	

RESULT 4

RESULT 4
US-09-968-653A-4
; Sequence 4, Application US/09968653A
; Publication No. US20030073084A1
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrey V
; Garkavstev, Igor
;

```

1 Riabowol, Karl
2 TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
3 Pathway
4
5 NUMBER OF SEQUENCES: 7
6 CORRESPONDENCE ADDRESSES:
7 ADDRESS: McDonnell Boehnen Hulbert & Berghoff
8 STREET: 300 South Wacker Drive
9 CITY: Chicago
10 STATE: Illinois
11 COUNTRY: USA
12 ZIP: 60606
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/968,653A
22 FILING DATE: 01-Oct-2001
23 CLASSIFICATION: <Unknown>
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/09/006,783A
27 FILING DATE: 15-JAN-1998
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: No. US20030073084Alnan, Kevin E
31 REGISTRATION NUMBER: 35,303
32 REFERENCE/DOCKET NUMBER: 97,837
33
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 312-913-0001
36 TELEFAX: 312-913-0002
37
38 INFORMATION FOR SEQ ID NO: 4:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 873 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: cDNA
45 FEATURE:
46 NAME/KEY: CDS
47 LOCATION: 7..813
48 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
49 US-09-968-653A-4
50

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[illegible]

Db 408 CAATGCGGATCGGTAGCGAGTCTGACAAAGCCCAACAGACGGCTCAGGGCGGAGCG 467
 QY 535 GACCACTGAAAGCCGTGATTTATGTACATGCGCAATGGGATTTGAAGACTGTGATGATCA 594
 Db 468 CAACAACGAGAACCGTGAGAACCGTCCAGCAACACGACGACGACGCGCTCGGG 527
 QY 595 GCACACTAAGAAAGAAATCCAAAGTCAGCAAGAAAGAAAGAAAGCTCCAAAGGCCAAGCA 654
 Db 528 CACACCAAGGAGAGAAAGCCCAAGACCTCCAAAGAAAGAGAGCGCTCCAAAGGCCAAGGC 587
 QY 655 GGAAGGAGAGCTTACCTGTTGAGTTTGCATAGATCTTAAAGACCTTACATAGCTT 714
 Db 588 GGAGGAGAGGCTCCCTCGGACCTCCCAAGCTCCCAAGCAAGACCTTACCTGCT 647
 QY 715 ATCAACCAAGTCTTATGGGAGATGATAGATGTGACATGAACAGTGTCCAATTGA 774
 Db 648 GTCAACCAAGTCTTATGGGAGATGATGCTCGGACAGGAGTGTCCCATCGA 707
 QY 775 ATGGTTTCACTTTTCAATGTGTTTCACTTACCTTAAACCAAGGGGAAATGGTATGCCC 834
 Db 708 GTGGTTTCACTTTTCTGCTGGGCTCAATCATAAACCAAGGGCAAGTGTGCTGCTC 767
 QY 835 AAAGTCAGGAGAGATAATGAGAAACAAATGGACAAAGTACTGAAAGACAAAAAGGA 894
 Db 768 CAAGTCCCGGGGAGAGAGAGAACCAATGGACAAAGCCCTGGAGAAATCCAAAAAGA 827
 QY 895 TAG 897
 Db 828 GAG 830

RESULT 5
 US-09-764-877-3454
 ; Sequence 3454, Application US/09764877
 ; Patent No. US20020147140A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC005
 ; CURRENT APPLICATION NUMBER: US/09/764,877
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 4031
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3454
 ; LENGTH: 8487
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-764-877-3454

Query Match 17.0%; Score 183.4; DB 10; Length 8487;
 Best Local Similarity 57.0%; Pred. No. 4e-34;
 Matches 395; Conservative 0; Mismatches 266; Indels 32; Gaps 2;
 QY 236 CAAGAACCTTAAAGAAATTTGATGATGCTACGAAAAATATTAAGAAAGATGATTTA 295
 Db 6229 CCAGAGATCCTGAAGGAGGTAGACGAGTCTACGAGCGCTTACGTCCGAGACAGACGGG 6288
 QY 296 AACCCAGAAGAACGCTACAGCAGCTTCTCCAGAGAGCAGCTAATTAATAGTCAAGAAATG 355
 Db 6289 GCGCAGAACGGCGGAGTGTGCACTGTGTGAGCGGCCCTGATCCGACGAGGAGCTG 6348
 QY 356 GGAGATGAAAAATACAGATTTGTTACAAAAATGCTGAAATGGTGGAAATCGGGCAAGA 415
 Db 6349 GCGCAGGAGAAGATCCAGATCGTGTAGCCAGATGGTGTGAGCTGGTGTGAGAACCGCAGCGG 6408
 QY 416 CAAATGGAGTTACACTACAGTGTTCCTCAAGATC----- 449
 Db 6409 CAGGTGGAGACCGACCTGGAGCTGTTCGAGGCGCAGCAGGAGGTGGCGACACAGCGGCG 6468
 QY 450 -----CTGCTGAAAGTGAACGAGCCCTCAGATAAGCAAAAGATGGATTCCAGCAACCA 504
 Db 6469 AACAGGGCAAGCTGCGCGGACAGACAGCCCAAGAGCGGAGCGGCGGAGCGGTGACAAG 6528

QY 505 AAGATCTTCAAGAAGACCCCGCAGGCGAGCGGACCACTGAAAGCCGTGATTTATGTACAT 564
 Db 6529 CCCAACAGCAAG-CGCTACGCGCGCAGCGCAACAGAGAACCGTGTGAGAACGCGTCCAG 6587
 QY 565 GCGAATGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAGAAATCCAAAGTCAGC 624
 Db 6588 CAACCAAGCAGCAGCAGCGCGGCTTCGCGGCACACCCAAAGGAGAGAACGCGCAAGACCTC 6647
 QY 625 AAAGAAAAGAACGCTCCCAAGGCCAAGCAGGAGGAGGAGCTTCACCTGTTGAGTTTCG 684
 Db 6648 CAGAAGAAGAGCGCTCCCAAGGCCAAGCGGAGGAGGAGGCTCCCTGCGGACCTCCC 6707
 QY 685 AATAGATCTTAAATGACCTTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGAT 744
 Db 6708 CATCGACCCCAAGCAACCCACGCTACTGTCTGTGCAACCAAGTGTCTTATGGGAGATGAT 6767
 QY 745 AGATGTGACATGAACAGTGTCCCAATTCATGATGATGATGATGATGATGATGATGATGAT 804
 Db 6768 CGGCTCGCAACAGCAGGAGTGTCCCATCGAGTGTGATGATGATGATGATGATGATGAT 6827
 QY 805 CTATAACCAAGGGGAAATGGTATTGCCCCAAAGTGCAGGGAGATAATGAGAAAAAAT 864
 Db 6828 TCATAAACCCAGGCGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 864
 QY 865 GGACAAAAGTACTGAAAGACAAAAAGGATAG 897
 Db 6888 GGACAAAAGCTGGAGAAATCCAAAAAGAGAG 6920

RESULT 6
 US-09-968-653A-2
 ; Sequence 2, Application US/09968653A
 ; Publication No. US20030073084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guckov, Andrey V
 ; Garkavstev, Igor
 ; Riabowol, Karl
 ; TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/968,653A
 ; FILING DATE: 01-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/006,783A
 ; FILING DATE: 15-JAN-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. US20030073084A1nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 97,837
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-0002
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2061 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
FILE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US/10/037,270
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 435
LENGTH: 1864
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (164)...(1420)
US-10-037-270-435

Query Match 8.5%; Score 91.6; DB 9; Length 1864;
Best Local Similarity 64.8%; Pred. No. 4.1e-12;
Matches 136; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 674 GTTGAGTTGGCAATAGATCCTAATGAACCTACATACCTGTTATGCAACCAAGTGTCTTAT 733
Db 1214 GTTGAGTTGGCAATAGATCCTAATGAACCTACATACCTGTTATGCAACCAAGTGTCTTAT 1273
QY 734 GGGAGATGATAGGATGTCACATGAACAGTGTCCCAATGAATGGTTTTCACATTTCATGT 793
Db 1274 GGTGAGATGGTGGATGTGATACCAAGATGTCCTATAGAAATGGTTTTCATGCTATGCTGC 1333
QY 794 GTTTCATTACCTATATAAAGCAAGGGGAAATGGTATGTCCTCAAGTGTCCAGGAGATAAT 853
Db 1334 GTTGAGTGCACAGAGCACCACCAAGGCAATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1393
QY 854 GAGAAACAAATGCAACAAAGTACTGAAAG 883
Db 1394 AAGAGAAGGCGCAGCAGACACAAATAAAGG 1423

RESULT 9

US-09-854-133-146
Sequence 146, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Henderson, Robert A.
APPLICANT: Mohamath, Raodoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10

CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 146
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapien
US-09-854-133-146

Query Match 7.7%; Score 83.6; DB 9; Length 451;
Best Local Similarity 58.6%; Pred. No. 1.5e-10;
Matches 163; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 169 CGTGAGTGCCTGCCCCACGACATGACAGGAGACGTGTCTGTCTGCTGCGAGAGCTGGACAA 228
Db 16 CATCGAGTCCCTTTCGACTTGCAGAGAAATGTCTCGCTGATGCGGGAGATCGACGC 75
QY 229 CAAATATCAAGAAACGTTAAAGAAATGATGATGTCTACGAAAAATATAAGAAAGA 288
Db 76 GAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGTCTACGAGCGCTTCAGTCCGCGAGAC 135
QY 289 TGATTTAAACACAGAAACGTTACAGCAGCTTCTCCAGAGAGCAGCTAAATTAATAGTCA 348
Db 136 AGACGGGGCGCAGAAAGCGCGGATGCTGCACCTGTGTGCGCGCGCTGATCCGCA-CCA 194
QY 349 AGAATTTGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTTGGTGGAAAAATCG 408
Db 195 GGAGCTGGCGCAGCAGAGATCCAGATCGTGAGCCAGATGTTGGAGCTGTTGGAGAACCG 254
QY 409 GCAAGACAAATGGAGTTACACTCACAGTGTTCGAAG 446
Db 255 CACGGCGCAGGTGGAGCCAGCCAGCTGTCGAGG 292

RESULT 10

US-09-738-973-146
Sequence 146, Application US/09738973
Patent No. US20020110563A1
GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Henderson, Robert A.
APPLICANT: Lodes, Michael J.
APPLICANT: Fling, Steven P.
APPLICANT: Mohamath, Raodoh
APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Indrias, Carol Yoseph
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 146
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapien
US-09-738-973-146

Query Match 7.7%; Score 83.6; DB 10; Length 451;
Best Local Similarity 58.6%; Pred. No. 1.5e-10;
Matches 163; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 169 CGTGAGTGCCTGCCCCACGACATGACAGGAGACGTGTCTGTCTGCTGCGAGAGCTGGACAA 228
Db 16 CATCGAGTCCCTTTCGACTTGCAGAGAAATGTCTCGCTGATGCGGGAGATCGACGC 75

Qy 229 CAATATCAAGAAAGTTAAAGAAATGATGTCTACGAAAAATATAGAAGAAGA 288
 Db 76 GAATACCAAGAGATCTGAAGAGCTAGAGAGTGTACGAGCGCTTCAGTCGGAGAC 135
 Qy 289 TGATTTAAACAGAGAAACGCTACAGAGCTTCTCCAGAGACACTAATTAATAGTCA 348
 Db 136 AGACGGGGCCAGAAAGCGGGGATGCTGCACTGTGTCAGCGCGCTGATCCGCA-CCA 194
 Qy 349 AGAATGGGAGATCAAAAATACAGATGTGTACACAATGCTCGAATTTGGTGAATCG 408
 Db 195 GGAGCTGGGACGAGAGATCCAGATCGTGAGCCAGATGTGGAGCTGGTGGAGACCG 254
 Qy 409 GGCAAGCAAAATGGAGTTACACTCACAGTGTTCCTCAAG 446
 Db 255 CACGCGCAGGTGGACAGCCACGTGGAGCTGTTCCAGG 292

RESULT 11

US-09-801-368-257
 ; Sequence 257, Application US/09801368
 ; Patent No. US20020128250A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busby, Robert
 ; APPLICANT: Cali, Brian
 ; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No. US20020128250A1man, Thea
 ; APPLICANT: Royer, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff
 ; APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 ; FILE REFERENCE: 109272.147
 ; CURRENT APPLICATION NUMBER: US/09/801.368
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 09/487,558
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/160,587
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 257
 ; LENGTH: 993
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-257

Query Match 6.2%; Score 66.6; DB 10; Length 993;
 Best Local Similarity 66.2%; Pred. No. 3.5e-06;
 Matches 96; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 Qy 698 GAACCTACATCTCTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGCAAAAT 757
 Db 835 GAACCGTCTACTGCTACTGTAAACCAAGTGCATACGGGAAATGGTGGGTGTGATGGC 894
 Qy 758 GAACAGTGTCAAATGAATGTTTCACCTTTTCATGTGTTCACCTTACCTATFAAACCAAG 817
 Db 895 GCAGACTGTGACGTAGAAATGTTCCATTTGCCATGTATTGGACTCGAAACTCTACCTAAG 954
 Qy 818 GGAATGGTATTGCCCAAAAGTCA 842
 Db 955 GGCAAGTGGTATTCCGACGACTGCA 979

RESULT 12

US-09-938-842A-1178
 ; Sequence 1178, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff
 ; APPLICANT: Krels, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/09/938.842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1178
 ; LENGTH: 813
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1178

Query Match 5.7%; Score 62; DB 9; Length 813;
 Best Local Similarity 65.1%; Pred. No. 4.1e-05;
 Matches 108; Conservative 0; Mismatches 55; Indels 3; Gaps 1;
 Qy 669 CACCTGTTGAGTTTGCATAGATCCTATGAACCTACATACCTGCTTATGCAACCAAGTGT 728
 Db 542 CAATGAAGAGCAGCCCAATCGATCCAAACGAACCACTTACTGTGCTGCCATCAGGTGT 601
 Qy 729 CTTATGGGAGATGATAGGATGTGACATGAACCAAGTGTGTC---CAATTGAATGTTTCACT 785
 Db 602 CCTTTGGAGACATGATTCCTGTGCAATGAGATGCAAGGAGGTGAATGTTTCACT 661
 Qy 786 TTTTCATGTTTCACTTACCTATTAACCAAGGGGAAATGTTATG 831
 Db 662 ATACATGCTTGGCTCACACCTGAGACCAAGATTCAAGGAAATG 707

RESULT 13

US-09-918-995-16047
 ; Sequence 16047, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918.995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 16047
 ; LENGTH: 456
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(456)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-16047

Query Match 5.3%; Score 56.8; DB 9; Length 456;
 Best Local Similarity 49.4%; Pred. No. 0.00053;
 Matches 179; Conservative 0; Mismatches 174; Indels 9; Gaps 1;
 Qy 94 GTACTGCTGCGCTCGGCTCCTGACCGGGAGCGCGGCTGCTCAGCTGCTAGTGCA 153
 Db 7 GNCCTCATTTGTCGNACCCCTAGTCCGTGTGGTGAATTCGCGACCGCCATGTACTTGA 66
 Qy 154 GGACTACTTGTGAGTGGTGGAGTGCCTGCCCCACGACATGCAGAGAACGTGTCTGTGCT 213

```
Db 67 GCACTATCGGACGATGATGAGAACCTTCCCTCGGAACCTTCAGAGAACTTCAGCTGAT 126
QY 214 GCGAGAGCTGGACAAACAAATATCAAGAAACGTTAAAGAAATGATGATCTTACGAAAA 273
Db 127 GCGAGAGCTGGACCAAGGACGGAAGATGAAGAGCAGAGATGACATCTGGCTCGAGA 186
QY 274 ATATAA-----GAAAGAGATGATTTAAACCAAGAAACGCTTACAGCAGCTTCT 324
Db 187 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAACGCGCTGGAGCGCTCGAGAAGAT 246
QY 325 CCAGAGACGACATTAATTAAGTCAAGAATGGGAGATGAAGAAATACAGATGCTTACACA 384
Db 247 CCAGAAGCGCTTACAGCAAGTGAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCA 306
QY 385 AATGCTCGAATGGTGGAAATCGGCAAGACAAATGGAGTTCACACTCACAGTGTTCACA 444
Db 307 GACCTACGAGATGGTGGATTAACACATTCGAGGCTTGATGCAGACCTGGCGGCTTTGA 366
QY 445 AG 446
Db 367 AG 368
```

RESULT 14

US-09-960-352-4582/c
; Sequence 4582, Application US/09960352
; Patent No. US20020137139A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

NUMBER OF SEQ ID NOS: 15112

LENGTH: 393

TYPE: DNA

ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 20-LIB3057-013-Q1-K1-E7

US-09-960-352-4582

Query Match 4.8%; Score 51.6; DB 10; Length 393;
Best Local Similarity 51.3%; Pred. No. 0.0089;
Matches 120; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

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QY 847 AGATAATGAGAAACAAATGACAAAAGTACTGAAAGACAAAAAGGATAGAGATCGAG 906
Db 387 AAAAAATAAAAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 328
QY 907 GTAGTAAGGCCATCCACATTTTAAGGGTTATTTCTCTTTTATATAATTCGTTGCTTT 966
Db 327 AATTTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 268
QY 967 CAGAAATGTTTAGGGTAAATGCAATGACATGCAATGCAATGCAATGCAATGCAATGCAAT 1026
Db 267 TAAAAATATATATTTAAAAATAATAATAATAATAATAATAATAATAATAATAATAATA 208
QY 1027 ATGGTGTATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
Db 207 AAATTATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 154
```

RESULT 15

US-09-919-580-114/c

; Sequence 114, Application US/09919580

; Patent No. US20020110832A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth

APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.552

CURRENT APPLICATION NUMBER: US/09/919,580

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 114

LENGTH: 361

ORGANISM: Homo sapiens

NAME/KEY: misc.feature

LOCATION: 49, 89, 101, 141, 209, 253, 305, 324, 331, 360

OTHER INFORMATION: n = A,T,C or G

US-09-919-580-114

Query Match 4.7%; Score 50.8; DB 10; Length 361;
Best Local Similarity 64.6%; Pred. No. 0.013;
Matches 73; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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QY 968 AGAAATGTTTGGTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1027
Db 124 ATAAAGATATTTTGGTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 65
QY 1028 TGGTGTATTAATAAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1080
Db 64 GTTGTATTAATAATTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 12
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Search completed: June 20, 2003, 02:45:35
Job time : 195 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 01:20:25 ; Search time 1533 Seconds
(without alignments)
11409.736 Million cell updates/sec

Title: US-09-513-365a-2

Perfect score: 1080

Sequence: 1 ggcgcgcgcgcgcgtcatg.....aaaaaaaaaaaaaaaaaaaa 1080

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_esti.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pin.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	812.8	75.3	1464	11	AK012716 Mus muscu
2	747.8	69.2	912	14	BO277444 AGENCOURT
3	735	68.1	735	14	BM982877 UI-CF-EN1
4	727.6	67.4	798	12	BG184056 RST2972 A
5	711	65.8	793	12	BE796780 601587557
6	694.2	64.3	778	13	BI548536 603191255

RESULT 1	AK012716	AK012716	1464 bp	mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:281001LM06:similar to P33ING2, full insert sequence.	linear	HTC 19-JAN-2002
LOCUS	AK012716	AK012716.1	GI:12849649	HTC; CAP trapper.		
DEFINITION	AK012716	AK012716.1	GI:12849649	Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library		
ACCESSION	AK012716	AK012716	AK012716	Mus musculus		
VERSION	AK012716	AK012716.1	GI:12849649			
KEYWORDS	AK012716	AK012716.1	GI:12849649			
SOURCE	AK012716	AK012716.1	GI:12849649			
ORGANISM	AK012716	AK012716.1	GI:12849649			
REFERENCE	AK012716	AK012716.1	GI:12849649			
AUTHORS	AK012716	AK012716.1	GI:12849649			
TITLE	AK012716	AK012716.1	GI:12849649			
JOURNAL	AK012716	AK012716.1	GI:12849649			
MEDLINE	AK012716	AK012716.1	GI:12849649			
PUBMED	AK012716	AK012716.1	GI:12849649			
REFERENCE	AK012716	AK012716.1	GI:12849649			
AUTHORS	AK012716	AK012716.1	GI:12849649			
TITLE	AK012716	AK012716.1	GI:12849649			
JOURNAL	AK012716	AK012716.1	GI:12849649			
MEDLINE	AK012716	AK012716.1	GI:12849649			
PUBMED	AK012716	AK012716.1	GI:12849649			

BG211544 RST31111
BM682789 UI-E-EJ1-
BM719460 UI-E-EJ1-
BI458873 df121d04.
BI091047 602855235
BI460319 603201967
AV647917 AV647917
AW674008 ba59f06.x
BE839427 RC3-FN014
BI546850 603189754
A1186701 qe82d12.x
BE839460 RC3-FN014
BF114684 7166c08.x
A1800614 wg12e12.x
A1458721 tk13h10.x
A1857399 w155f09.x
A1883642 w159h01.x
BQ206861 UI-R-D21-
BI458874 df121d04.
AA746304 oa56d03.r
BF732679 nae05d11.
BF513151 UI-H-BW1-
BE831862 RC6-MT006
AA797495 vw28b01.r
BG189892 RST8946 A
A1818729 wk91d10.x
AW52211 wy87d06.x
BQ033210 UI-1-CF0-
A1126389 qc55ell.x
A1204672 zr87c06.r
BF523624 UI-R-C1-1
BI132471 AR031G10L
AW674790 ba59f06.y
A1453008 tj51e06.x
BI676689 1c53a06.x
BE773058 RC1-FT013
BQ746746 UI-M-FA0-
BF222230 7p55e10.x
BF732979 nae07a03.

ALIGNMENTS

RESULT 1	AK012716	AK012716	1464 bp	mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:281001LM06:similar to P33ING2, full insert sequence.	linear	HTC 19-JAN-2002
LOCUS	AK012716	AK012716.1	GI:12849649	HTC; CAP trapper.		
DEFINITION	AK012716	AK012716.1	GI:12849649	Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library		
ACCESSION	AK012716	AK012716	AK012716	Mus musculus		
VERSION	AK012716	AK012716.1	GI:12849649			
KEYWORDS	AK012716	AK012716.1	GI:12849649			
SOURCE	AK012716	AK012716.1	GI:12849649			
ORGANISM	AK012716	AK012716.1	GI:12849649			
REFERENCE	AK012716	AK012716.1	GI:12849649			
AUTHORS	AK012716	AK012716.1	GI:12849649			
TITLE	AK012716	AK012716.1	GI:12849649			
JOURNAL	AK012716	AK012716.1	GI:12849649			
MEDLINE	AK012716	AK012716.1	GI:12849649			
PUBMED	AK012716	AK012716.1	GI:12849649			
REFERENCE	AK012716	AK012716.1	GI:12849649			
AUTHORS	AK012716	AK012716.1	GI:12849649			
TITLE	AK012716	AK012716.1	GI:12849649			
JOURNAL	AK012716	AK012716.1	GI:12849649			
MEDLINE	AK012716	AK012716.1	GI:12849649			
PUBMED	AK012716	AK012716.1	GI:12849649			

Db 720 CCAATTGAATGGCTTTCACATTTTCATGCTGCTTCACTTACCTATATAAACCAGGGGAAAT 779

QY 825 GTATTGCCCCAAAGTCAGGGGAGATAAATGAGAAACAA 863

Db 780 GGTATTGCCACAGTCGAGGGGAGATATGGAGAAA 818

BM982877 735 bp mRNA linear EST 21-MAR-2002

UI-CF-EN1-acs-d-05-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone

UI-CF-EN1-acs-d-05-0-UI 3', mRNA sequence.

BM982877

BM982877.1 GI:19606826

EST.

human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 735)

TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477

COMMENT Contact: McCray, PB

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..735

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-CF-EN1-acs-d-05-0-UI"

/clone_lib="UI-CF-EN1"

/tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.

TAG_LIB=UI-CF-EN1

TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS

6hr to LPS 24h

TAG_SEQ=CTGCTCAGGT

BASE COUNT 180 a 161 c 114 g 280 t

ORIGIN

Query Match 68.1%; Score 735; DB 14; Length 735;

Best Local Similarity 100.0%; Pred. No. 2.4e-102;

Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 ATTAATAGTCAAGAATTTGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTG 397

Db 735 ATTAATAGTCAAGAATTTGGAGATGAAAAAATACAGATTGTTACACAAATGCTCGAATTG 676

QY 398 GTGAAAAATCGGGCAAGACAAATGGAGTTTACACTCACAGTGTGTTTCCAAAGATCTGCTGAA 457

Db 675 GTGAAAAATCGGGCAAGACAAATGGAGTTTACACTCACAGTGTGTTTCCAAAGATCTGCTGAA 616

QY 458 AGTGAACGAGCCTCAGATAAAGCAAGATGGATTCCAGCCACCAAGAAAGATCTTCAAGA 517

Db 615 AGTGAACGAGCCTCAGATAAAGCAAGATGGATTCCAGCCACCAAGAAAGATCTTCAAGA 556

QY 518 AGACCCCGCAGCGCAGCGGACCTGTTTATGTCACATGGCAATGGGATT 577

Db 555 AGACCCCGCAGCGCAGCGGACCTGTTTATGTCACATGGCAATGGGATT 496

QY 578 GAAGACTGTGTATGATCAGCCACCTAAAGAAAAAGAAATCCAAAGTCAGCAAGAAAAAGAA 637

Db 495 GAAGACTGTGTATGATCAGCCACCTAAAGAAAAAGAAATCCAAAGTCAGCAAGAAAAAGAA 436

QY 638 CGCTCCAAGGCCAAGCAGGAGGAAAGCTTCACCTGTTGAGTTTGCATAGATCTTAAT 697

Db 435 CGCTCCAAGGCCAAGCAGGAGGAAAGCTTCACCTGTTGAGTTTGCATAGATCTTAAT 376

QY 698 GAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGACAAAT 757

Db 375 GAACCTACATACCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGACAAAT 316

QY 758 GAACAGTGTCCAAATGAATGGTTTCACTTTTCAATGTGTTTCACTTACCTATAAACCAAG 817

Db 315 GAACAGTGTCCAAATGAATGGTTTCACTTTTCAATGTGTTTCACTTACCTATAAACCAAG 256

QY 818 GGAATGTGTATGTCCTCAAGTCAGGGGAGATAATCAGAAAAACAATGGAACAAGTACT 877

Db 255 GGAATGTGTATGTCCTCAAGTCAGGGGAGATAATCAGAAAAACAATGGAACAAGTACT 196

QY 878 GAAAGACAAAAAAGGATAGAGATCGAGTAGTAAAGGCCATCCACATTTTAAAGGGTT 937

Db 195 GAAAGACAAAAAAGGATAGAGATCGAGTAGTAAAGGCCATCCACATTTTAAAGGGTT 136

QY 938 ATTTGCTTTTATATAATTCGTTTTCAGAAAAATGTTTATAGGTAATGATGATAGAC 997

Db 135 ATTTGCTTTTATATAATTCGTTTTCAGAAAAATGTTTATAGGTAATGATGATAGAC 76

QY 998 TATGCAATATTTTAAATCATTAGTATTAATGCTGTATTAAAGAGTTGTTGCTACTTTGAA 1057

Db 75 TATGCAATATTTTAAATCATTAGTATTAATGCTGTATTAAAGAGTTGTTGCTACTTTGAA 16

1058 AAAAAAAGAAAAA 1072

15 AAAAAAAGAAAAA 1

RESULT 4

BM984056/c

LOCUS

DEFINITION RST2972 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BM984056

VERSION BM984056.1 GI:13705743

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 798)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random

JOURNAL
MEDLINE
COMMENT

activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9300
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 531.
Location/Qualifiers
1. 798

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries Using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT 197 a 178 c 130 g 293 t
ORIGIN

Query Match 67.4%; Score 727.6; DB 12; Length 798;
Best Local Similarity 98.9%; Pred. No. 3.1e-101;
Matches 785; Conservative 0; Mismatches 4; Indels 5; Gaps 5;

QY 261 ATGCTCTAGCAAAATATAGAAAGACAGATGATTTAAACCCAGAGAAACGGTCTACAGCAGC 320
DB 789 ATGCTCTACGCAAAATAT-AGAAAGAGATGATTTAAACCCAGAGAAACGGTCTACAGCAGC 731
QY 321 TTCTCCAGAGACGACCTAATTAATAGTCAGAATGGGAGATGAATAACATACAGATCTTA 380
DB 730 TTCTCCAGAGACGACCT-ATTATAGTCAGAATGGGAGATGAATAACATACAGATCTTA 674
QY 381 CACAATGCTCGAATTTGGTGGAAATCGGGCAAGACAAATGGAGTTACACTCAGCTGTT 440
DB 673 CACAATGCTCGAATTTGGTGG-AAATCGGGCAAGACAAATGGAGTTACACTCAGCTGTT 615
QY 441 TCCAAGATCTGCTGAAGTGAACGAGCCTCAGATGAAGCAAGATGGATTCAGGCAAC 500
DB 614 TCCAAGATCTGCTGAAGTGAACGAGCCTCAGATGAAGCAAGATGGATTCAGGCAAC 555
QY 501 CAGAAAGATCTTCAAGAGACCCCGCAGGCGAGCCAGTGAAGCCGCTGATTTATGTC 560
DB 554 CAGAAAGATCTTCAAGAGACCCCGCAGGCGAGCCAGTGAAGCCGCTGATTTATGTC 495
QY 561 ACATGGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAAGT 620
DB 494 ACATGGCAATGGGATTTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAAGT 435
QY 621 CAGCAAGAAAAGAAACGCTCAAGCCAGCAGGAGGAGGAGCTTACCTGTTGAGT 680
DB 434 CAGCAAGAAAAGAAACGCTCAAGCCAGCAGGAGGAGGAGCTTACCTGTTGAGT 375
QY 681 TTGCAATAGATCTTAATGAACCTACATCTGCTTATGCAACCAAGTCTTTATGGGAGA 740
DB 374 TTGCAATAGATCTTAATGAACCTACATCTGCTTATGCAACCAAGTCTTTATGGGAGA 315
QY 741 TGATAGGATGTGACAAATGAACAGTGTCCAAATTTGAATGGTTTTCATTTTCATGTGTTTAC 800
DB 314 TGATAGGATGTGACAAATGAACAGTGTCCAAATTTGAATGGTTTTCATTTTCATGTGTTTAC 255
QY 801 TTACCTATAAACCAAGGGGAAATGGTATTTGCCCAAGTGCAGGGGAGATGAATGAGAAA 860
DB 254 TTACCTATAAACCAAGGGGAAATGGTATTTGCCCAAGTGCAGGGGAGATGAATGAGAAA 195
QY 861 CAATGACAAAAGTACTGAAAACACAAAAGATAGAGATCGAGGTAGTAAAGGCCAT 920
DB 194 CAATGACAAAAGTACTGAAAACACAAAAGATAGAGATCGAGGTAGTAAAGGCCAT 135

QY 921 CCACATTTTAAAGGGTATTGCTCTTTTATATATATGCTTTGCTTTTTCAGAAAATGTTT 980
DB 134 CCACATTTTAAAGGGTATTGCTCTTTTATATATATGCTTTGCTTTTTCAGAAAATGTTT 75
QY 981 GGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
DB 74 GGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 15
QY 1041 GTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1054
DB 14 GTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1

RESULT 5

BE796780

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM794 row: a column: 16

High quality sequence stop: 769.

Location/Qualifiers

1. 793

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3941655"

/clone_lib="NIH.MGC.7"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/notes="Organ: lung; Vector: pOTB7; Site: 1; XhoI; Site: 2;

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average.

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 240 a 177 c 230 g 146 t

ORIGIN

Query Match 65.8%; Score 711; DB 12; Length 793;

Best Local Similarity 98.9%; Pred. No. 1e-98;

Matches 747; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 1 GCGGCG 60

DB 41 GCGGCG 100

QY 61 GCGGCG 120

DB 101 GCGGCG 160

QY 121 GCGGCG 180

optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"

/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTACGGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAAGT; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJ1
TAG_TISSUE=Foveal and Macular Retina
TAG_SEQ=GTCC"

BASE COUNT 164 a 148 c 110 g 253 t
ORIGIN
Query Match 62.2%; Score 671.8; DB 14; Length 675;
Best Local Similarity 99.7%; Pred. No. 9.6e-93;
Matches 673; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 398 GTGGAATTCGGGCAAGACAAATGGAGTTTACACTCACAGTGTTCACAGATCTCTGTGAA 457
DB 675 GTGGAATTCGGGCAAGACAAATGGAGTTTACACTCACAGTGTTCACAGATCTCTGTGAA 616
QY 458 AGTGAACGAGCTCAGATTAACCAAGATGGATTCCAGCCACCAAGATGCTTCAAGA 517
DB 615 AGTGAACGAGCTCAGATTAACCAAGATGGATTCCAGCCACCAAGATGCTTCAAGA 556
QY 518 AGACCCCGCAGCAGCGGACCAAGTGAAGCCGTGATTATGTACATGCAATGGGATT 577
DB 555 AGACCCCGCAGCAGCGGACCAAGTGAAGCCGTGATTATGTACATGCAATGGGATT 496
QY 578 GAAGACTGTGATGATCAGCCACTTAAGAAAAGAAATCAAGTCAGCAAGAAAAGAA 637
DB 495 GAAGACTGTGATGATCAGCCACTTAAGAAAAGAAATCAAGTCAGCAAGAAAAGAA 436
QY 638 CGCTCAAGGCCAAGCAGGAAGGAGCTTCACTTGTGATGTTGCAATAGATCTTAT 697
DB 435 CGCTCAAGGCCAAGCAGGAAGGAGCTTCACTTGTGATGTTGCAATAGATCTTAT 376
QY 698 GAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAT 757
DB 375 GAACCTACATCTGCTTATGCAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAT 316
QY 758 GAACAGTGTCCAAATGAAGTGTTCACCTTTTCATGTTTCACTTACCTATTAACCAAG 817
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QY 818 GGGAAATGTTATGCTCCCAAGTGCAGGGGAGATATAGAAAACAAATGGACAAAGTACT 877
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QY 938 ATTGCTCTTTATATAATTCGTTTCTTTCAGAAAATGTTTAAAGGTAATGCAATAGAC 997
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RESULT 9
LOCUS BM719460
DEFINITION UI-E-EJ1-af-g-22-0-UI-r1 UI-E-EJ1 Homo sapiens cDNA clone
ACCESSION UI-E-EJ1-af-g-22-0-UI 5', mRNA sequence.
VERSION BM719460
KEYWORDS BM719460.1 GI:19038113
SOURCE EST.
ORGANISM human.

REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 664)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)

JOURNAL Program for Rat Gene Discovery and Mapping
MEDLINE Contact: Soares, MB
COMMENT 9704477
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="UI-E-EJ1"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site.1: EcoR I; Site.2: Not I;
UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTACGGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAAGT; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 241 a 111 c 149 g 162 t
ORIGIN
Query Match 61.4%; Score 663; DB 14; Length 664;
Best Local Similarity 99.8%; Pred. No. 2.1e-91;
Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

BASE COUNT

Db	154	TAGTAAAGGCATCCACATTTTAAAGGGTTATTGTCTTTTATATAAATCGTTGCTTC	95
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Qy	1028	TGCTGTATTAAAAAGTTTGTCTACTTTTGAAAAA	1061
Db	34	TGCTGTATTAAAAAGTTTGTCTACTTTTGAAAAA	1
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LOCUS	BE839427/c		
DEFINITION	RC3-FN0143-190700-022-d12 FN0143 Homo sapiens cDNA, mRNA sequence.	564 bp	linear EST 22-SEP-2000
ACCESSION	BE839427		
VERSION	BE839427.1	GI:10271805	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1. (bases 1 to 564)		
	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,		
	Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,		
	Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,		
	Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare		
	M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and		
	Simpson,A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed		
JOURNAL	sequence tags		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
COMMENT	20202663		
	Contact: Simpson A.J.G.		
	Ludwig Institute for Cancer Genetics		
	Rua Pruf. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,		
	Brazil		
	Tel: +55-11-2704922		
	Fax: +55-11-2707001		
	Email: asimpson@ludwig.org.br		
	This sequence was derived from the FAPESP/LICR Human Cancer Genome		
	Project. This entry can be seen in the following URL		
	(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t3-RC3-FN0143-190		
	700-022-d12&t3-2000-07-19&t4-1)		
	Seq primer: puc 18 forward		
	High quality sequence start: 18		
	High quality sequence stop: 564.		
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	/clone_lib="FN0143"		
	/dev_stage="Adult"		
	/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI		
	; Site_2: SmaI; A mini-library was made by cloning		
	products derived from ORESTES PCR (U.S. Letters Patent		
	application No. 196,716 - Ludwig Institute for Cancer		
	Research) profiles into the puc 18 vector. Reverse		
	transcription of tissue mRNA and cDNA amplification were		
	performed under low stringency conditions."		
BASE COUNT	108 a 156 c 121 g 179 t		
ORIGIN			
Query Match	51.3%; Score 554.2; DB 12; Length 564;		
Best Local Similarity	99.5%; Pred. No. 7e-75;		
Matches	556; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
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Qy	98	TCGTCGGCTCGGCTCCTGACCGGGAGCGGAGCGGGTGTCTACCTGCTACGTGCAGGAC	157
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Qy	218	GAGCTGGACACAAATATCAAGAAACGTTAAAGGAAATTTGATGTCTACGAAAAATAT	277
Db	384	GAGCTGGACACAAATATCAAGAAACGTTAAAGGAAATTTGATGTCTACGAAAAATAT	325
Qy	278	AAGAAAGAGATGATTTAAACCAAGAAACGTTCTACAGCAGCTTCTCCAGAGAGCACTA	337
Db	324	AAGAAAGAGATGATTTAAACCAAGAAACGTTCTACAGCAGCTTCTCCAGAGAGCACTA	265
Qy	338	ATTAATAGTCAAGATTTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG	397
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Qy	398	GTGAAAAATCGGCAAGACAAATGGAGTTACACTCACAGTGTTCCTCAAGATCCTGCTGAA	457
Db	204	GTGAAAAATCGGCAAGACAAATGGAGTTACACTCACAGTGTTCCTCAAGATCCTGCTGAA	145
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Qy	518	AGACCCCGCAGCGAGCGGACCGAGTGAAGCGGTGATTTATGTCACATGGCAAAATGGGATT	577
Db	84	AGACCCCGCAGCGAGCGGACCGAGTGAAGCGGTGATTTATGTCACATGGCAAAATGGGATT	25
Qy	578	GAAGACTGTGATGATCAGC	596
Db	24	GAAGACTGTGATGAGCACC	6

Search completed: June 20, 2003, 02:40:38
Job time : 1538 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2003, 01:18:10 ; Search time 295 seconds
(without alignments)
8244.604 Million cell updates/sec

Title: US-09-513-365A-2

Perfect score: 1080

Sequence: 1 gcggccgcggccggtgcatg.....aaaaaaaaaaaaaaaaaaaa 1080

Scoring table: IDENTITY/LNUC
Gapop 10|0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1080	22	AAD12783 Tumour suppressor
2	1046	96.9	1078	20	AAZ08596 Human ING1L encodi
3	838.4	77.6	840	20	AAZ08595 Human ING1L encodi
4	825.2	76.4	1153	21	AAZ47473 Human tumour suppr
5	332.2	30.8	346	21	AAC28459 Human secreted pro
6	325	30.1	325	21	AAZ47474 Human tumour suppr
7	253.6	23.5	2817	21	AAZ53790 Murine P37ING1 codi
8	237.4	22.0	1911	21	AAZ53792 Human P37ING1 codi
9	236	21.9	1533	22	AAH28478 Nucleotide sequenc

10	236	21.9	2897	24	ABK86977 Human inhibitor of
11	197.2	18.3	1835	21	AAZ53789 Murine Ing1 common
12	183.8	17.0	1143	22	AAH28479 Nucleotide sequenc
13	183.8	17.0	1902	18	AAH28479 Nucleotide sequenc
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16	183.8	17.0	2061	19	AAV62285 Tumour suppressor
17	183.8	17.0	2061	19	AAV62285 Tumour suppressor
18	183.8	17.0	2061	19	AAV62285 Tumour suppressor
19	183.8	17.0	2061	19	AAV62285 Tumour suppressor
20	183.8	17.0	2061	19	AAV62285 Tumour suppressor
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27	183.8	17.0	2061	19	AAV62285 Tumour suppressor
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ALIGNMENTS

RESULT 1
AAD12783

ID AAD12783 standard; DNA; 1080 BP.

AC AAD12783;

DT 23-OCT-2001 (first entry)

XX Tumour suppressor homologue protein, p33ING2 DNA.

DE Tumour suppressor; p47ING3; cell proliferation; cellular aging; p33ING2;
KW anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.

XX Unidentified.

OS XX
FH XX
CDs XX
Key Location/Qualifiers
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/*tag= a
/product= "Tumour suppressor homologue protein, p33ING2"

XX WO200159114-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04425.

XX 09-FEB-2000; 2000US-0181292.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Harris CC, Nagashima M;

XX

DR WPI: 2001-488975/53.
 XX P-PSDB; AAE06675.
 PT New tumor suppressor protein p47ING3 for the diagnosis and treatment of
 PT tumors -
 XX
 XX
 XX
 XX Disclosure; Page 78; 80pp; English.
 PS
 CC The present sequence is a DNA encoding tumor suppressor homologue
 CC protein, p33ING2 which is homologous to human tumor suppressor protein,
 CC p47ING3. The tumor suppressors of the invention are involved in the
 CC regulation of cell proliferation and in the control of cellular aging,
 CC anchorage dependence and apoptosis. The tumor suppressor protein,
 CC p47ING3, nucleic acids encoding it and antibodies against it are useful
 CC for diagnosis, prevention and treatment of tumours and cancers. The
 CC p47ING3 DNA is also used in gene therapy.
 XX
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 Best Local Similarity 100.0%; Pred. No. 1.5e-236;
 Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 721 CCAAGTGTCTTATGGGAGATGATGAGTGTGACAAATGAACAGTGTCCAAATGAATGGTT 780
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 ID AAZ08596 standard; cDNA; 1078 BP.
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 AC AAZ08596;
 XX
 DT 18-OCT-1999 (first entry)
 XX
 DE Human ING1L encoding cDNA with 5' and 3' untranslated regions.
 XX
 KW Human; TSC403; ING1L; diagnosis; lung cancer; cell cycle; regulation;
 KW cell proliferation; cell aging; apoptosis; tumour suppressor; ss.
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 OS Homo sapiens.
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 FH Key
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 PD 12-AUG-1999.
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 PF 02-FEB-1999; 99WO-JP00419.
 XX
 PR 28-APR-1998; 98JP-0134679.
 PR 03-FEB-1998; 98JP-0038133.
 PR 05-MAR-1998; 98JP-0073234.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Horie M, Nagata M, Ozaki K, Shimada Y;
 XX
 DR WPI; 1999-494294/41.
 DR P-PSDB; AAY29606.
 XX
 PT Human lung-specific gene TSC430 overexpressed in cancer tissue, used
 PT for treatment of, e.g. colon tumour.
 XX
 PS Claim 15; Page 91-93; 99pp; Japanese.
 XX
 CC The present sequence represents the human tumour suppressor gene ING1L.
 CC The present invention also describes the human gene TSC403 expressed
 CC specifically in normal lung tissue. TSC403 is useful in the
 CC diagnosis, investigation and treatment of cancers in which it
 CC overexpressed, including cancer of the lung, breast, fallopian tube,
 CC oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas.
 CC ING1L is useful in the investigation of cell proliferation, aging and
 CC apoptosis and the pathology of cancer, the diagnosis and treatment of

QY 68 ATGTTAGGGCAGCAGCAGCAACTGTACTCTCGGTGCGCTCTACCGGGAGCGG 127

Db 720 AAGAAACGCTCCAGGCCAAGCAGGAAAGGAGCTTACCTGTTGAGTTGCAATAGA 779
 Qy 691 TCCTAATGAACCTACATACCTGCTTATGCAACCAAGTCTTATGGGAGATGATAGATG 750
 Db 780 TCCTAATGAACCTACATACCTGCTTATGCAACCAAGTCTTATGGGAGATGATAGATG 839
 Qy 751 TGCAATGAACGCTGCTCAATGAATGGTTTCACTTTTCATGTTTCACTTACCTATAA 810
 Db 840 TGCAATGAACGCTGCTCAATGAATGGTTTCACTTTTCATGTTTCACTTACCTATAA 899
 Qy 811 ACCAAGGGGAATGGTATTGCCCAAGTGCAGGGAGATTAATGAGAAACAATGGACAA 870
 Db 900 ACCAAGGGGAATGGTATTGCCCAAGTGCAGGGAGATTAATGAGAAACAATGGACAA 959
 Qy 871 AAGTACTGAAAGACAAAAAGGATAGAGATCAGGTAGTAAAGGCCATCCACATTTTA 930
 Db 960 AAGTACTGAAAGACAAAAAGGATAGAGATCAGGTAGTAAAGGCCATCCACATTTTA 1019
 Qy 931 AAGGTTATTGCTTTTATATATATTCGTTTTCGTTTTCAGAAATGTTTAGGTTAATGC 990
 Db 1020 AAGGTTATTGCTTTTATATATATTCGTTTTCGTTTTCAGAAATGTTTAGGTTAATGC 1079
 Qy 991 ATAAGACTATGCAATATTTTATATATATTCGTTTTCGTTTTCAGAAATGTTTAGGTTAATGC 1050
 Db 1080 ATAAGACTATGCAATATTTTATATATATTCGTTTTCGTTTTCAGAAATGTTTAGGTTAATGC 1139
 Qy 1051 TTTGAAAAAATAA 1064
 Db 1140 TTTGAAAAAATAA 1153

RESULT 5

AAAC28459
 ID AAC28459 standard; CDNA; 346 BP.
 AC AAAC28459;
 XX
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 32534.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; CDNA isolation;
 KW gene therapy; chromosome mapping, ss.
 XX
 XX Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000EP-0200610.
 XX
 XX 26-FEB-1999; 99US-0122487.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX Claim 1; SEQ ID 32534; 71pp + CD-ROM; English.
 XX
 XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences

CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 346 BP; 130 A; 63 C; 80 G; 70 T; 3 other;
 Query Match 30.88; Score 332.2; DB 21; Length 346;
 Best Local Similarity 99.18; Pred. No. 3.2e-66;
 Matches 343; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 Qy 254 ATTGATGATGCTACGAAAAATATAAGAAAGAGATGATTTAAACCAAGAAACGCTCA 313
 Db 1 ATTGATGATGCTACGAAAAATATAAGAAAGAGATGATTTAAACCAAGAAACGCTCA 60
 Qy 314 CAGCAGCTTCTCCAGAGAGACACTAATTAATAGTCAAGAAATGGGAGATGAAAAATACAG 373
 Db 61 CAGCAGCTTCTCCAGAGAGACACTAATTAATAGTCAAGAAATGGGAGATGAAAAATACAG 120
 Qy 374 ATTGTTACACAAATGCTCGAATGGTGGAAAAATCGGCAAGACAAATGGAGTTACACTCA 433
 Db 121 ATTGTTACACAAATGCTCGAATGGTGGAAAAATCGGCAAGACAAATGGAGTTACACTCA 180
 Qy 434 CAGTGTTCCTCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATGGATTCC 493
 Db 181 CAGTGTTCCTCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAGATGGATTCC 240
 Qy 494 AGCCAACCAAGAAAGATCTTCAAGAAAGACCCCGCAGGCGGACCCAGTGAAGCCGTGAT 553
 Db 241 AGCCAACCAAGAAAGATCTTCAAGAAAGACCCCGCAGGCGGACCCAGTGAAGCCGTGAT 300
 Qy 554 TT-ATGTCACATGCGAAATGGGATTGAAGACTGTGATGATCAGCCA 598
 Db 301 THNNTGTACATGGCAATGGGATTGAAGACTGTGATGATCAGCCA 346

RESULT 6

AAZ47474/C
 ID AAZ47474 standard; CDNA; 325 BP.
 XX
 AC AAZ47474;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human tumour suppressor (TUSUP) fragment nucleotide sequence.
 XX
 KW Tumour suppressor protein; TUSUP; human; cancer; treat; prevent;
 KW reproductive tract; gastrointestinal tract; immune system; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO9961612-A1.
 XX
 PD 02-DEC-1999.
 XX
 XX 20-MAY-1999; 99WO-US11136.
 XX
 XX 28-MAY-1998; 98US-0086359.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Tang YT, Corley NC, Patterson C;
 XX
 XX WPI; 2000-062711/05.
 XX
 XX New human tumour suppressor protein for treating cancer, particularly of
 PT reproductive and gastrointestinal tracts or immune system -
 XX
 XX Disclosure; Page 64; 71pp; English.
 XX

Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ING1 gene, each having their own promoter have been discovered. Expression of one promoter (1a) produces a protein identical to ING1. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated p37ING1 (Wild type: p33ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ING1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ING1 or its antisense sequence can identify individuals expressing the oncogenic form of ING1. Novel peptide sequences taken from the 104 N-terminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and studying cancers.

[illegible][illegible]

145	Qy	CTAGTGTCCAGGACTTACCTTGAGTTCGGTGGAGTGCCTGCCCCACACATGCAGAGGAACGT	204
86	Db	CTATGTGGGGAGCTTACCTGGACTCCATCGAGTCCCTGCTTTCGACTTGCAGAGAAATGT	145
205	Qy	GTCTGTGCTCGGAGAGCTGGACACAAATATCAGAAACGTTAAAGGAAATTTGATGATGT	264
146	Db	CTCGCTGATCGGGAGATCGACGCGAATACCAAGAGATCCTGAAGGAGCTAGACGAGTG	205
265	Qy	CTACGAAAATATAGAAAGAAGATGATTTAAACCAGAANAAGCTCTACAGCAAGCTTCT	324
206	Db	CTACGAGCGCTTCAGTCCGAGACAGACGGGGCGGCGAGAACGGCGGATGTCGCACTGTG	265
325	Qy	CCAGAGGACCTAATTAATAGTCAAGAATTTGGGAGATGAAATAATACAGATTTGTATACACA	384
266	Db	GCAGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGNAGATCCAGATCGTAGCCCA	325
385	Qy	AATGCTCGAATTTGTTGGAAATCGGGCAAGACAATGGAGTTACACTCACAGTGTTTTCCA	444
326	Db	GATGGTGGAGCTGTTGGAGAACCCGACCGCGCAGTGGACAGCCACCGTGGAGCTGTTCGA	385
445	Qy	AGATC-----CTGCTGAAAGTGAACGAGCCTCAGATA	476
386	Db	GGCGCAGCAGGAGCTGGGGCACAGTGGGCACAGCGGCNAGTTTGGCGGGACAGGCC	445
477	Qy	AAGCAAAAGATGGATTCCAGGCCAACCCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG	534
446	Db	CAATGGCGATCGGCTAGCGAGCTGTGACAAGCCCCAACAGACGCTCAGCGCGGCACGC	505
535	Qy	GACCAGTGAAGCCGCTGATTTATGTCATATGGCAATTTGGGATTTCAAACACTGTGTATGATCA	594
506	Db	CAACACGAGAACCTTGTGAGAACCGCTCCAGCAACCCAGCACGACACGCGGCGCTCGGG	565
595	Qy	GCACCTTAAAGAAAGAAATCCAAGTTCAGCAAGAAAAAAGAAACCGTCCCAAGGCCAAGCA	654

86	CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTTTCGACTTTCGACAGAAAATGT	145
205	GTCTGTGCTCGGAGAGCTGGACACAAATATCAGAAACGCTTAAAGAAATTTGATGATGT	264
146	CTCGCTGATCGGGAGATCGACGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTG	205
265	CTACGAAAAATATAAGAAAGAAGATGATTTAAACCCAGAAGAAACGCTCAGACGAGCTTCT	324
206	CTACGAGCGCTTCAGTCCGAGACAGACGGGGCCGACAAGCGCGGATGCTGCACGTGTGT	265
325	CCAGAGAGCACTAATTAAATAGTCAAGAATTTGGGAGATGCAAAAAATACAGATTTGTTACACA	384
266	GCAGCGCGCTGATCCGCGACGCCAGGAGCTGGCGCGAGAGAAGATCCAGATCGTGAGCCA	325
385	AATGCTCGAATTTGGTGTAAAAATCGGGCAAGACAAATGGAGTTACACTCAGAGTGTTTCCA	444
326	GATGGTGGAGCTGGTGGAGAACCCGACCGCGCAGTGGACAGCCACGCTGGAGCTGTTTCCA	385
445	AGATC-----CTGCTGAAAGTGAACAGCGCCCTCAGATA	476
386	GGCGCACGAGGAGCTGGCGGACACAGCTGGGCAACAGCGGCNAAGTTGGCGGGACAGGCC	445
477	AAGCAAAAGATGGATTCCAGCCCAACGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG	534
446	CAATGGCGATCGGCTAGCGCAGTCTGACAAGCCCCAACAGCAAGCGCTCAGCGCGGCAGCG	505
535	GACCAAGTAAAGCCGTGATTTATGTCATATGGCAAAATGGGATTTCAAACACTGTGATGATCA	594
506	CAACACGAGAAACGCTGAGAACCGGCTCCAGCAACCCAGCAGCACGACGCGCGCTCGGG	565
595	GCACCTTAAAGAAAGAAATCCAGTTCAGCAAGAAAAAGAAACGCTCCCAAGGCCAAGCA	654

205	QY	GTCTGTGCTCGGAGAGCTGCACACAATATCAAGAAACGTTTAAGAGAAATTTGATGATGT	264
146	Db	CTCGCTGATCGGGAGATCGACGGCAATATCAAGAAGATCTTGAAGGAGCTAGACGAGTG	205
265	QY	CTACGAAAAATATAAGAAAGAAGATGATTTAAACCCAGAAGAAACGTTACAGCAGCTTCT	324
206	Db	CTACGAGCGCTTCAGTCGCGAGACAGACGGGGCCAGAAAGCGGCGATCTGCACCTGTG	265
325	QY	CCAGAGAGCACTAATTTAATAGTCAAGAAATTTGGGAGATGAAAAAAATACAGATTTGTACACA	384
266	Db	GCAGCGCGCGTGTATCCGCGACGCCAGGAGAGCTGGGCGCGAGAAAGATCCAGATCTGTGAGCCA	325
385	QY	AATGCTCGAATTTGGTGGAAATCGGCGCAAGCAAAATGAGGTTACACTCACAGTGTTTCCA	444
326	Db	GATGGTGGAGCTGGTGTGAGAACCCGACCGCGCAGTGGACAGCCACCTGGAGCTGTTTCCA	385
445	QY	AGATC-----CTGCTGAAAGTGAACAGAGCCCTCAGATA	476
386	Db	GGCCGACGAGGCTGGGGCACACAGTGGCAACAGCGGCAAGTTGGCGGGACGCC	445
477	QY	AAGCAAAAGATGGATTCCAGCCCAACCGAAGATCTTCAAGAAGACCCCGCAG--GCAGCG	534
446	Db	CAATGGCGATCGCGTAGCGCAGTCTGTACAAGCCCAACAGCAAGCGCTCAGCGCGGCACGC	505
535	QY	GACCAGTGAAGCCGTGATTATGTCATCGGCAAAATGGGATTTCAAGACACTGTGATGATCA	594
506	Db	CAACACGAGAAACGTTGAGAACCGGTCCAGCAACCCAGCACGACGCGCGCTCGGG	565
595	QY	GCCACCTTAAAGAAAGAAATCCAAAGTCAGCAAAAGAAAAAGAAACGCTTCCAAAGGCCAAGCA	654

146	CTCCTGATGGGGAGATCAGCGCAATACCAAGAGATCCTGAAGGAGCTAGACGAGT	205
265	CTACGAAAAATATAAGAAAGAAGATGATTTAAACCCAGAAACGTTCTACAGCAGCTTCT	324
206	CTACGAGCGCTTCAGTCGCGAGACAGCGGGCGCAGAAAGCGCGGATGCTGCACCTGTGT	265
325	CCAGAGAGCACTAATTAATAGTCAAGAAATTTGGGAGATCAAAAAATACAGATTGTTACACA	384
266	GCAGCGCGCGTGTATCCGCGACGCCAGGAGCTGTGGCGAGCAGAGAATCCAGATCGTAGGCCA	325
385	AATGTCGAATTGGTGTGAAAAATCGGCAAGACAATGGAGTTACACTCACAGTCTTTTCCA	444
326	GATGGTGGAGCTGGTGAGAAACCCACGCGCGCAGGTGGACAGCCACGCTGGAGCTGTTCGA	385
445	AGATC-----CTGTGAAAGTGAACGAGCCTCAGATA	476
386	GGCGCAGCAGGAGCTGGCGGACACAGTGGGCAACAGCGGCAAGTTTGGCGGGACGCC	445
477	AAGCAAGATGGATTCCAGGCCAACGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG	534
446	CAATGGCGATCGGTACGCGAGTCTGACAAGCCCAACAGAACGGCTCAGCGCGGCACGC	505
535	GACCAGTGAAGCCGTATTATGTCACATGGCAAAATGGGATTGAACACACTGTGATGATCA	594
506	CAACACGAAACCGTGAGAACCGGTCCAGACCCAGCACCGACGCGCGCTCGGG	565
595	GCCACCTAAAGAAAGAAATCCAAGTCAGCAAAAGAAAAAGAAACGCTCCAAAGGCCAAGCA	654

Db	206	CTAGGAGCGCTT	CAGTCGCGAGACAGACGGGCGCAAGCGCGGATGCTGCAC	TGTGT	265
Qy	325	CCAGAGAGCACT	TAATTAATAGTCNAGAATTTGGGAGATGAAAAATACAGATTGTTACACA	384	
Db	266	GCACGCGCGCT	TGATTCGCGACGCCAGGAGCTGGCGCGAGAGAAGATTCAGATCGTAGGCCA	325	
Qy	385	AATGCTCGAAT	TGGTGGAAAATCGGCGAAGCAAAATGGAGTTACACTCACAGTCTTTCCA	444	
Db	326	GATGGTGGAGCT	TGGTGGAAAATCGGCGAAGCAAAATGGAGTTACACTCACAGTCTTTCCA	444	
Qy	445	AGATC-----	-----CTGCTGAAGTGAAGGAGCCTCAGATA	476	
Db	386	GGCGCAGCAGG	AGCTGGGCGCACACAGTGGGCACAGCGGCAAGGTTGGCCGGCAGACGCC	445	
Qy	477	AAGCAAAAGAT	GATTCCAGCCCAACCAAGAAAGATCTTCAAGAAAGACCCCGCAG--GCAGCG	534	
Db	446	CAATGGCGAT	CGGTACGCGAGTCTGACAAGGCCCAACAGCAAGCGCTCACGGCGCGCAGCG	505	
Qy	535	GACCAGTGAAG	CCGCTGATTTATGTCACTGGCGAAATGGGATTTGAAACACTGTGATGATCA	594	
Db	506	CAACACGAGAAC	CGTGGAGAACGGTCCAGCAACGACGACCAACGACGCGCGCTCGGG	565	
Qy	595	GCCACCTTAA	AGAAAAGAAATCCAAGTTCAGCAAGAAAAAGAAACGCTTCCAAGGCCCAAGCA	654	

Qy	325	CGAGAGCAGCTAATTAATAGTCNAGAAATTCGGGAGATGAAAAATACAGATTGTTACACA	384
Db	266	GCAGCGCGCGCTGATTCGCGACGCCAGGAGCTGGCGCGAGAGAAGATCCAGATCGTGAGGCCA	325
Qy	385	AATGCTCGAATTTGTTGAAAAATCGGGCAAGACAAATGGAGTTTACACACAGCTTTTCCA	444
Db	326	GATGGTGGAGCTGTTGTGAGAACCGCACGCGCAGTGGACAGGCCACGTGGAGCTGTTCGA	385
Qy	445	AGATC-----CTGCTGAAGTGAAGGAGCCTCAGATA	476
Db	386	GGCGCAGCAGGAGCTGGCGCACAGTGGGCACAGCGGCAAGGTTGGCGCGGACAGGCC	445
Qy	477	AAGCAAAAGATGGATTCCAGCCCAACCGAAGAAATCTTCAAGAAAGACCCCGCAG--GCAGCG	534
Db	446	CAATGGCGATCGGCTAGCGCAGTCTGACAAGGCCCAACAGCAAGCGCTCAGGCGCGCAGCG	505
Qy	535	GACCAAGTGAACCGCTGATTTATGTCATATGGGCAAAATGGGATTCAAGACACTGTGATGATCA	594
Db	506	CAACACGAGAAACCGTGTAGGAACCGCTCCAGCAACGACCCACAGCAGCGCGCTCGGG	565
Qy	595	GCCACCTTAAAGAAAAGAAATCCAAGTTCAGCAAGAAAAAAGAAACGCTCCAAAGGCCCAAGCA	654

Db	266	GCAGCGCGCGCTGATCGCAGCCAGGAGCTGGGCGCAGAGAAGATCCAGATCTGTGAGCCA	325
Qy	385	AATGCTCGAAATGGTGGAAAATCGGCAAGACAATGGAGTTACACTCAGACGTGTTTCCA	444
Db	326	GATGTGGAGCTGGTGGAGAAACCGCAGCGCGCAGTGGACAGCCACGTGGAGCTGTTCGA	385
Qy	445	AGATC-----CTGCTGAAGTGAACGAGGCTTCAGATA	476
Db	386	GGCGCAGCAGGAGTGGGCGACACAGTGGGCAACAGCGGCAAGGTTTGGCGCGACAGGCC	445
Qy	477	AAGCAAAAGATGGATTCTTCAGGCCAACCAAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG	534
Db	446	CAATGGCGATGCGGTAGCGCAGTCTGACAAGCCCAACAGCAAGCGTCAAGCGCGCAGCG	505
Qy	535	GACCAGTGAAGCGCTGATTATTGTCACATGCGCAATGGGATTCAAGACACTGTGATGATCA	594
Db	506	CAACACGAGAACCGCTGAGAACCGCTCCAGCAACCGACACACAGCAGCGCGCTCGGG	565
Qy	595	GCACCTTAAAGAAAGAAATCCAGTTCAGCAAGAAAAAGAAAGCGTCCAAAGGCCAAGCA	654

[illegible][illegible]

Qy	445	AGATC-----CTGCTGAAGTGAACGAGCCTCAGATA	476
Db	386	GGCGCAGCAGGAGCTGGCGCACACAGTTGGCAACAGCGCAAGTTGGCGCGACAGGCC	445
Qy	477	AAGCAAAGATGGATTCCAGGCCAACGAAAGATCTTCAAGAAGACCOCGCAG--GCAGCG	534
Db	446	CAATGGCGATCGGTAGCGCAGTCTGACAAGCCCCAAGCAAGACGGCTCAGCGCGCGCAGCG	505
Qy	535	GACCAGTGAAAGCCGTATTATTGTCACATGGCAAAATGGGATTGAACACACTGTGATGATCA	594
Db	506	CACACAGCAGAACCGTGAAGACCGGTCCAGCAACCCAGCACGACGCGCGCTCGGG	565
Qy	595	GCCACCTTAAGAAAAGAAATCCAAGTCAGCAAGAAAAAGAAACCGCTCCAAGGCCCAAGCA	654

Db	386	GGCGCAGCAGGAGCTGGCGGCACACAGTGGCGCAACAGCGGCAAGGTTTGGCGCGGACAGCC	445
Qy	477	AAGCAAGATGGATTCCAGCCCAACCAAGAAGATCTTCAAGAAAGACCCCGCAG--GCAGCG	534
Db	446	CAATGGCGATGCGGTACGCGAGCTGTACAAGCCCAACGACGAACGCGCTCACGGCGGCGACGC	505
Qy	535	GACCAGTGAAGCGGTGATTATTGTGCATATGGCAAAATGGGATTTCAGACACTGTGTATGATCA	594
Db	506	CACAACGAGAACCGTGAGAACCGGTCCAGCAACCGACACCGCGCGCTCGGG	565
Qy	595	GCCACCTAAAGAAAGAAATCCAAGTCAGCAAGAAAAAGAAACCGCTCCAAGGCCCAAGCA	654

[illegible]

Accession	Sequence	Position
Db	CAATGGCGATGCGGTAGCGAGTCTGACAAAGCCCAACAGAACGCTCACGGCGGCGACGG	505
Qy	GACCACTGAAAGCCGCTGATTATTGTCACATGGCAATGGGATTCAAGACACTGTGATGATCA	594
Db	CAACAACGAAACCGTGAGAACGGTCCAGCAACGACGACCAACGACGCGCGCTCGGG	565
Qy	GCCACCTTAAAGAAAGAAATCCAAAGTCAGCAAGAAAAAGAAAGACCGTCCAAAGGCCCAAGCA	654

Qy	535	GACCA	GTAAG	CCGCT	GATTT	TATG	TCA	TGG	CAAA	TGGG	ATTC	CAAC	ACACT	TGT	GAT	GATCA	594
Db	506	CAACA	CGAGA	CCGT	GAGAC	CGGT	CCAG	CA	ACC	CAC	CGC	AC	CAG	CGC	GCG	CTCGG	565
Qv	595	GCCAC	CTTAA	AGAAA	AGAAAT	CCAA	GTC	AGCA	AGAAAA	AGAAAC	CGCT	TCCA	AGG	CCCA	AGCA	AGCA	654

595 GCCACCTTAAGAAAGAAATCCAAGTCAGCAAGAAAAAGAAACGGCTCCAGGCCAAGCA 654

Db 575 GCTGGACACGACGAGTGGCCCCATCGAGTGGTTCCTCCACTTCTCGTGGCGTGGGCTCAATC 634
 Qy 807 ATAAACCAAGGGGAAATGGTATTCGCCAAAGTCGAGGGGAGATAATGAGAAAACAATGG 866
 Db 635 ATAAACCAAGGGGCAAGTGGTACTGTCCCAAGTGGCGGGGGAGAACGAGAACCATGG 694
 Qy 867 ACAAAAGTACTGAAAGACCAAAAAGGATAG 897
 Db 695 ACAAGCCCTGGAGAAATCCAAAAGAGAG 725

RESULT 15

AAAT69652
 ID AAAT69652 standard; cDNA; 2061 BP.

AC AAAT69652;

DT 27-AUG-1997 (first entry)

DE Tumour suppressor gene INGI full-length cDNA.

XX Tumour suppressor gene; INGI; p33INGI; breast cancer; brain cancer;
 KW diagnosis; gene therapy; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 16..900

FT primer_bind /tag= a

FT complement (474..494)

FT /tag= b

FT /note= "direct primer 1"

FT complement (763..782)

FT /tag= c

FT /note= "direct primer 2"

FT primer_bind 857..876

FT /tag= d

FT /note= "reverse primer 3"

FT primer_bind 890..900

FT /tag= e

FT /note= "reverse primer 4"

XX WO9721809-A1.

XX 19-JUN-1997.

XX 06-DEC-1996; 96WO-CA00819.

XX 15-NOV-1996; 96US-0751230.

XX 08-DEC-1995; 95US-0569721.

XX (UYTE-) UNIV TECHNOLOGIES INT INC.

XX Garkavstev I, Riabowol K;

XX WPI; 1997-332781/30.

XX P-PSDB; AAW18119.

XX Isolated tumour suppressor gene, INGI - useful to develop products
 PT for inhibiting or increasing cell proliferation, in particular for
 PT treatment or diagnosis of cancer

XX Claim 11; Fig 3; 63pp; English.

XX A full-length cDNA clone (AAAT69652), designated INGI, codes for a
 CC novel 33 kDa tumour suppressor protein p33INGI (AAW19119), formerly
 CC p33IGL, that is a potent inhibitor of cell growth. A partial clone
 CC (AAAT69651) was isolated by subtractive hybridisation between normal
 CC mammary and transformed epithelial cDNAs, isolation of an antisense
 CC INGI cDNA insert that caused increased cell proliferation, and use
 CC of the insert to screen normal human fibroblast and HeLa cDNA
 CC libraries. The complete INGI sequence was then obt'd. by 5'RACE.
 CC INGI is localised to the 13q33-34 chromosome region, to which a

CC number of human cancers have been mapped. INGI nucleic acids can
 CC be used in the diagnosis of breast cancer; a decreased level of
 CC INGI mRNA indicates cancerous cells. They can also be used in gene
 CC therapy methods to block the proliferation of cancer cells.
 XX
 SQ Sequence 2061 BP; 602.A; 439 C; 515 G; 505 T; 0 other;

Query Match 17.0%; Score 183.8; DB 18; Length 2061;
 Best Local Similarity 57.0%; Pred. No. 4.2e-32;
 Matches 394; Conservative 0; Mismatches 267; Indels 30; Gaps 2;

Qy 237 AAGAAACGTTAAAGGAATTTGATGATCTACGAAAAATATAGAAAGATGATTTAA 296
 Db 194 AACAGATCTGAAGGAGCTAGACGAGTGTCTAGCAGCGCTTTCAGTCGAGACAGAGGGG 253
 Qy 297 ACCAGAAAGACGCTCTACAGCAGCTTCTCCAGAGAGACACTAATTAATAGTCAAGATTGG 356
 Db 254 CGCAGAACGGCGGATGTGCACTGTGTGACGCGCGCTGATCCGAGCCAGGAGCTGG 313
 Qy 357 GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTTGGTGGAAATCGGGCAAGAC 416
 Db 314 CGCAGGAGAAGATCCAGATCGTGTGAGCCAGATGTTGAGCTGTGTGAGAACCCGACGCGC 373
 Qy 417 AAATGGAGTTACACTACAGTGTGTTCCAGATC----- 449
 Db 374 AGGTGGACAGCCACGCTGGAGCTGTTTCGAGGCGCACAGGAGCTGGGCGCACAGTGGCA 433
 Qy 450 -CTGCTGAAAGTGAACGAGCGCTCAGATAAAGCAAGATGGATTCAGCCCAACAGCAAGAA 508
 Db 434 ACAGCGCAAGTTGGCGGACAGGCGCCATGGCGTACGCGAGTGTGACAGC 493
 Qy 509 TCTTCAAGAA--GACCCCGCAGCGACGAGCAGTGAAGCGCGTATTATGTCACATGG 566
 Db 494 CCAACAGCAAGCGCTCACGGCGCAGCGCAACACAGAGACCGTGAGAAGCGGTCCAGCA 553
 Qy 567 CAATGGGATTGAAGACTGTGATGATCAGCCACTTAAGAAAGAAATCCCAAGTCAAGCA 626
 Db 554 ACCAGCACACGACGACGCGCGCTCGGGCACACACCAAGGAGAGGCGTCCCTGCCACCTCC 613
 Qy 627 AGAAAAAGAAAGCGTCCCAAGCGCAGAGGAGGAGGAGGAGTTCACCTGTTGAGTTGAA 686
 Db 614 AGAAGAAAGGCGCTCCCAAGGCGCAAGGCGGAGGAGGCGTCCCTGCCACCTCCCA 673
 Qy 687 TAGATCCTTAATGAACCTACATACCTTATGCAACCAAGTGTCTTTATGGGAGATGATAG 746
 Db 674 TCGACCCCAACGACCCACGTAATGATGATGATGATGATGATGATGATGATGATGATG 733
 Qy 747 GATGTGACAATGAACAGTGTCCCAATGATGATGATGATGATGATGATGATGATGATGATG 806
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Search completed: June 20, 2003, 01:27:32
 Job time : 299 secs

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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/db_xref="taxon:9606"
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LOCUS Homo sapiens p33 (ING2) mRNA, complete cds.
DEFINITION AF053537
ACCESSION AF053537
VERSION AF053537.1 GI:9992837
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1080)
AUTHORS Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P.,
Pedoux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C.
TITLE DNA damage-inducible gene p33ING2 negatively regulates cell
proliferation through acetylation of p53
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
MEDLINE 21396501
PUBMED 11481424
REFERENCE 2 (bases 1 to 1080)
AUTHORS Nagashima, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg. 37 Rm. 2C01,
Bethesda, MD 20892, USA
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LOCUS
DEFINITION Homo sapiens INGIL mRNA for INGILp, complete cds.
ACCESSION AB012853

1078 bp mRNA linear PRI 18-MAR-1999

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AB012853.1 GI:4115554
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Shimada, Y., Saito, A., Suzuki, M., Takahashi, E. and Horie, M.
Cloning of a novel gene (INGIL) homologous to ING1, a candidate
tumor suppressor
Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998)
2 (bases 1 to 1078)
Shimada, Y., Saito, A. and Horie, M.
Direct Submission
Submitted (07-APR-1998) to F. Yoshikazu Shimada, Otsuka Pharmaceutical
Co. Ltd., Otsuka GEN Research Institute, Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan
(E-mail: shim@otsuka.genome.ad.jp, Tel: 81-886-65-2888 (ex. 2476),
Fax: 81-886-37-1035)
Sequence updated (17-Apr-1998).
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VERSION AF062748.1 GI:9992841
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS Nagashima,M., Hagiwara,K., Minter,A.R. and Harris,C.C.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Dr. Bldg.37, Rm.2C26,
Bethesda, MD 20892, USA
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VERSION AC107214.4 GI:20128734
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 189972)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 189972)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,

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MO 63108, USA
 3 (bases 1 to 189972)
 Waterston, R. H.
 Direct Submission
 Submitted (10-APR-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Apr 10, 2002 this sequence version replaced gi:18677601.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Contact: submissions@wustl.wustl.edu
 ----- Project Information -----
 Center project name: H_NH0367N14

----- Summary Statistics -----
 Sequencing vector: M13, 0%
 Sequencing vector: plasmid, 100%
 Chemistry: Dye-terminator ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 189941 bases at least Q40
 Consensus quality: 190973 bases at least Q30
 Consensus quality: 191699 bases at least Q20
 Insert size: 204000; agarose-fp
 Insert size: 195974; sum-of-contigs
 Quality coverage: 11.39 in Q20 bases; agarose-fp
 Quality coverage: 10.96 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 8 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 1353: contig of 1847 bp in length
 * 3193: gap of unknown length
 * 3299: gap of unknown length
 * 3300: contig of 1121 bp in length
 * 4421: gap of unknown length
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 * 5658: gap of unknown length
 * 5759: gap of unknown length
 * 6866: gap of unknown length
 * 6967: contig of 30151 bp in length
 * 37117: gap of unknown length
 * 37218: contig of 64185 bp in length
 * 101403: gap of unknown length
 * 101503: 189972: contig of 88470 bp in length.

FEATURES
 source

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 Best Local Similarity 99.6%; Pred. No. 3.8e-165;
 Matches 819; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY	473	GATAAAGCAAGATGGATTCCAGCCAAACCAAGAAAGATCTTCAAGAAAGACCCCGCAG	532
DB	146945	GATAAAGCAAGATGGATTCCAGCCAAACCAAGAAAGATCTTCAAGAAAGACCCCGCAG	147004
QY	533	CGGACCAAGTGAAGCCCGTATTATGTGCATGCAATGGGATTTGAAGACTGTGATGAT	592
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QY	593	CAGCACCTAAAGAAAAAGAAATCCAAAGTCAAGAAAGAAAAAGAAACGCTCAAGGCCAAG	652
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VERSION	AF078834.1	GI:10039542			
KEYWORDS					
SOURCE	Mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1001)				
TITLE	Nagashima, M., Hagiwara, K., Hancock, A.R. and Harris, C.C.				
JOURNAL	Direct Submission				
FEATURES	Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, National Institutes of Health, 37 Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA				
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Db	361 AATGGAGCTGCATTCACAGTGTGTTCCAGATCTGCTGAAAGTGAACGAGCCCTCAGACAA 420				
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 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G., and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 168245)
 Worley,K.C.
 Direct Submission
 Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GZCX
 Center clone name: CH230-129P3
 ----- Summary Statistics
 Sequencing vector: Plasmid;
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 115858 bases at least Q40
 Consensus quality: 122576 bases at least Q30
 Consensus quality: 127679 bases at least Q20

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 50 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 148193 148192: contig of 11439 bp in length
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TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

* 148194 148293: gap of unknown length
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AC114762/c

LOCUS

DEFINITION

AC114762

AC114762

AC114762.2

GI:19703333

HTG; HTGS_PHASE1.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Waterston,R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 42029)

Waterston,R.H.

Direct Submission

Submitted (11-MAR-2002)

Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

3 (bases 1 to 42029)

Waterston,R.H.

Direct Submission

Submitted (25-MAR-2002)

Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Mar 25, 2002 this sequence version replaced gi:19339148.

COMMENT

Center: Washington University Genome Sequencing Center

Web site: http://genome.wustl.edu/gsc/index.shtml

Contact: submissions@wustl.edu

Project Information

Center project name: H_NH0366M05

NOTE: This is a 'working draft' sequence. It currently

consists of 26 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

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	Matches 577;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
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QY	293	TTAAACCAAGAAACGCTACAGCAGCTTCTCCAGAGAGCAGCTAAATTAATAGTCAAGAA	352		
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	Best Local Similarity	84.7%;	Pred. No. 4.8e-113;		
	Matches 577;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
QY	233	TATCAAGAAACGTTAAAGGAAATTCATGATGTCTACGAAAAATATAAGAAAGAGATCAT	292		
DB	15179	TTTTTAGAAACGTTAAAGGAAATTCATGATGTCTACGAAAAATATAAGAAAGAGATCAT	15120		
QY	293	TTAAACCAAGAAACGCTACAGCAGCTTCTCCAGAGAGCAGCTAAATTAATAGTCAAGAA	352		
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ACCESSION	AY014017	Xenopus laevis p3ZINGL mRNA,	complete cds.	
VERSION	AY014017.1	GI:17864714		
KEYWORDS	.			
SOURCE	Xenopus laevis.			

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Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
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Weinstock,G., and Gibbs,R.
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information
Center project name: GBVT
Center clone name: CH230-6112
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Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 137386 bases at least Q40
Consensus quality: 145233 bases at least Q30
Consensus quality: 150556 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 69 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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REFERENCE  1 (bases 1 to 840)
AUTHORS    Rancourt,D. and Garkavtsev,I.
TITLE      Structural organization and expression pattern of the murine INCL
gene
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 840)
AUTHORS    Garkavtsev,I.V.
TITLE      Direct Submission
JOURNAL    Submitted (11-MAY-1999) Genome Therapeutics Corp., 100 Beaver St.,
Waltham, MA 02453, USA

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